

Figure 1: Map of pVAXDCIB68 and cloning strategy

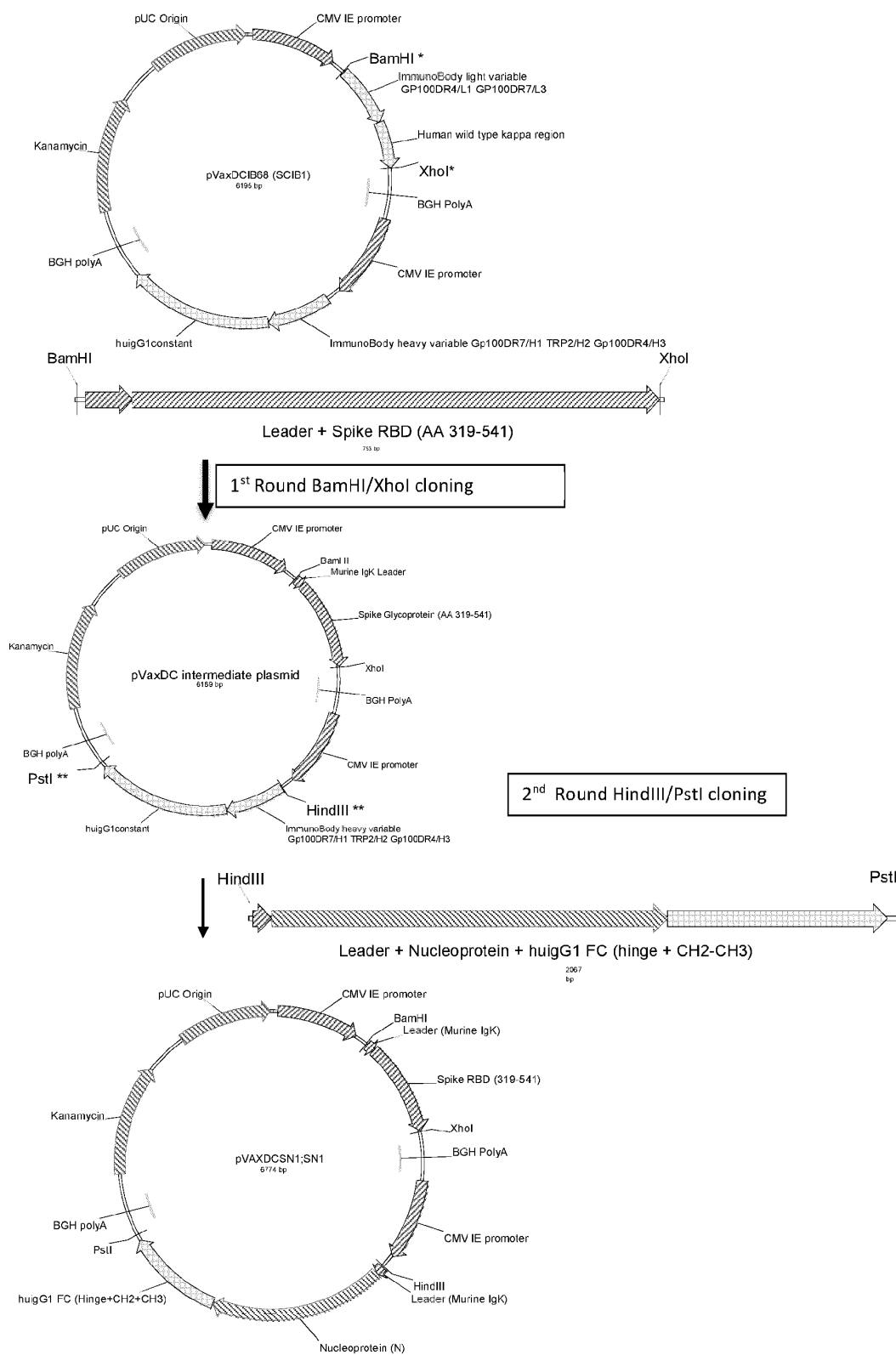


Figure 2: Sequence of pVAXDCSN1; SN1

A: Murine IgK Leader + Spike Glycoprotein (AA 319-541) (SEQ ID NO: 81)

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BamHI      M E T D T L L L W V L L L W V P
GGATCCGGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTTATTGTGGGTTCCTCC
1  -----!-----!-----!-----!-----!-----! 60

      G S T G R V Q P T E S I V R F P N I T N
      GGTTC AACCGGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCAACATCAGCAAC
61  -----!-----!-----!-----!-----!-----! 120

      L C P F G E V F N A T R F A S V Y A W N
      CTGTGCCCTTCGGCGAGGTGTTCAACGCCACCGAGATTGCCAGCGTGACGCCTGGAAC
121 -----!-----!-----!-----!-----!-----! 180

      R K R I S N C V A D Y S V L Y N S A S F
      AGGAAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTC
181 -----!-----!-----!-----!-----!-----! 240

      S T F K C Y G V S P T K L N D L C F T N
      AGCACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAAC
241 -----!-----!-----!-----!-----!-----! 300

      V Y A D S F V I R G D E V R Q I A P G Q
      GTGTACGCCGACAGCTTCGTGATCAGAGCGCAGAGGTGAGACAGATCGCCCCGGCCAG
301 -----!-----!-----!-----!-----!-----! 360

      T G K I A D Y N Y K L P D D F T G C V I
      ACCGGCAAGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATC
361 -----!-----!-----!-----!-----!-----! 420

      A W N S N N L D S K V G G N Y N Y L Y R
      GCGTGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTCTACAGA
421 -----!-----!-----!-----!-----!-----! 480

      L F R K S N L K P F E R D I S T E I Y Q
      CTGTTTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAG
481 -----!-----!-----!-----!-----!-----! 540

      A G S T P C N G V E G F N C Y F P L Q S
      GCCGGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGC
541 -----!-----!-----!-----!-----!-----! 600

      Y G F Q P T N G V G Y Q P Y R V V V L S
      TACGGCTTCCAGCCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTCTGAGC
601 -----!-----!-----!-----!-----!-----! 660

      F E L L H A P A T V C G P K K S T N L V
      TTCGAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCAAGAAGAGCACCAATCTGGTG
661 -----!-----!-----!-----!-----!-----! 720

      K N K C V N F * XhoI
      AAGAACAAGTGCGTGAACTTCTGATGACTCGAG
721 -----!-----!-----!-----!-----! 753

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B: Murine IgK Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 82)

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HindIII      M E T D T L L L W V L L L W V P
AAGCTTGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTTATTGTGGGTTCCTCC
1  -----!-----!-----!-----!-----!-----! 60

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Figure 2 continued

G S T G S D N G P Q N Q R N A P R I T F
GGTTCAACCGGCAGCGACAACGGCCCCCAGAACAGAGAAACGCCCCCAGAATCACCTTC
61 -----!-----!-----!-----!-----!-----! 120

G G P S D S T G S N Q N G E R S G A R S
GGCGGCCCCAGCGACAGCACCGGCAGCAACCAGAACGGCGAGAGAAGCGCGCCAGAAGC
121 -----!-----!-----!-----!-----!-----! 180

K Q R R P Q G L P N N T A S W F T A L T
AAGCAGAGAAGACCCAGGGCCTGCCAACAAACACCGCCAGCTGGTTCACCGCCCTGACC
181 -----!-----!-----!-----!-----!-----! 240

Q H C K E D L K F P R G Q G V P I N T N
CAGCACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGCCCATCAACACCAAC
241 -----!-----!-----!-----!-----!-----! 300

S S P D D Q I G Y Y R R A T R R I R G G
AGCAGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGC
301 -----!-----!-----!-----!-----!-----! 360

D G K M K D L S P R W Y F Y Y L G T G P
GACGCCAAGATCAAGCACCTGACCCCCAGATGCTACTTCTACTACCTGGGCACCGCCCC
361 -----!-----!-----!-----!-----!-----! 420

E A G L P Y G A N K D G I I W V A T E G
GAGGCCCGCCTGCCCTACGGCGCCAAACAGGACGGCATCATCTGGGTGGCCACCGAGGGC
421 -----!-----!-----!-----!-----!-----! 480

A L N T P K D H I G T R N P A N N A A I
GCCCTGAACACCCCCAAGGACCACATCGGCACCAGAAACCCCGCAACAACGCCGCCATC
481 -----!-----!-----!-----!-----!-----! 540

V L Q L P Q G T T L P K G F Y A E G S R
GTGCTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGA
541 -----!-----!-----!-----!-----!-----! 600

G G S Q A S S R S S S R S R N S S R N S
GGCGGCAGCCAGGCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGC
601 -----!-----!-----!-----!-----!-----! 660

T P G S S R G T S P A R M A G N G G D A
ACCCCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCT
661 -----!-----!-----!-----!-----!-----! 720

A L A L L L L D R L N Q L E S K M S G K
GCCCTGSCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAG
721 -----!-----!-----!-----!-----!-----! 780

G Q Q Q Q G Q T V T K K S A A E A S K K
GGCCAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCGAGGCCAGCAAGAAG
781 -----!-----!-----!-----!-----!-----! 840

P R Q K R T A T K A Y N V T Q A F G R R
CCCAGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGA
841 -----!-----!-----!-----!-----!-----! 900

G P E Q T Q G N F G D Q E L I R Q G T D
GGCCCCGAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCGAC
901 -----!-----!-----!-----!-----!-----! 960

Y K H W P Q I A Q F A P S A S A F F G M
TACAAGCACTGGCCCCAGATCGCCCACTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATG
961 -----!-----!-----!-----!-----!-----! 1020

S R I G M E V T P S G T W L T Y T G A I
AGCAGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGCGCCATC
1021 -----!-----!-----!-----!-----!-----! 1080

Figure 2 continued

K L D D K D P N F K D Q V I L L N K H I
AAGCTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATC
1081 -----!-----!-----!-----!-----!-----! 1140

D A Y K T F P P T E P K K D K K K K A D
GAGCCCTACAAGACCTTCCCCCACCAGGCCCAAGAAGGACAAGAAGAAGGCCGAC
1141 -----!-----!-----!-----!-----!-----! 1200

E T Q A L P Q R Q K K Q Q T V T L L P A
GAGACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

A D L D D F S K Q L Q Q S M S S A D S T
GCCGACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACC
1261 -----!-----!-----!-----!-----!-----! 1320

Q A E P K S C D K T H T C P P C P A P E
CAGGCCGAGCCCAATCGTGCATATAAACGCATACGTGCCCCCCTGTCCAGGCCCAGAG
1321 -----!-----!-----!-----!-----!-----! 1380

L L G G P S V F L F P P K P K D T L M I
TTGCTGGCTGGACCGAGCGTGTCTCTTCCCCCAAGGCCAAGCAGACCCCTCATCATC
1381 -----!-----!-----!-----!-----!-----! 1440

S R T P E V T C V V V D V S H E D P E V
AGCAGAACCCCGAGGTGACCTGCGTGGTGGTGGAGCTGAGCCACGAGGACCCCGAGGTG
1441 -----!-----!-----!-----!-----!-----! 1500

K F N W Y V D G V E V H N A K T K P R E
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAGAGAG
1501 -----!-----!-----!-----!-----!-----! 1560

E Q Y N S T Y R V V S V L T V L H Q D W
GAGCAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGTGACCCAGGACTGG
1561 -----!-----!-----!-----!-----!-----! 1620

L N G K E Y K C K V S N K A L P A P I E
CTGAACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAG
1621 -----!-----!-----!-----!-----!-----! 1680

K T I S K A K G Q P R E P Q V Y T L P P
AAGACCATCAGCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTGTACACCTGCCCCCC
1681 -----!-----!-----!-----!-----!-----! 1740

S R D E L T K N Q V S L T C L V K G F Y
AGCAGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTGAAGGGCTTCTAC
1741 -----!-----!-----!-----!-----!-----! 1800

P S D I A V E W E S N G Q P E N N Y K T
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACC
1801 -----!-----!-----!-----!-----!-----! 1860

T P P V L D S D G S F F L Y S K L T V D
ACCCCCCCTGTGTCGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGAC
1861 -----!-----!-----!-----!-----!-----! 1920

K S R W Q Q G N V F S C S V M H E A L H
AAGAGCAGATGGCAGCAGGGCAACGTGTTCTCTTGCAGCGTGATGCACGAGGCCCTGCAC
1921 -----!-----!-----!-----!-----!-----! 1980

N H Y T Q K S L S L S P G K *
AACCCTACACCCAGAAGAGCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGA
1981 -----!-----!-----!-----!-----!-----! 2040

PstI
ATTGCCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----! 2067

Figure 3: Sequence of pVAXDCSN2; SN2

A: Murine IgK Leader + Spike Glycoprotein (AA 319-541) + GS linker + Fibrin Trimer Motif (SEQ ID NO: 83)

BamHI M E T D T L L L W V L L L W V P
GGATCCGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTATTGTGGGTTCCTCC
1 -----!-----!-----!-----!-----!-----! 60

G S T G R V Q P T E S I V R F P N I T N
GGTTCAACCGGCAGAGTGCAGCCACCGAGAGCATCGTGAGATCCCCAACATCACCAAC
61 -----!-----!-----!-----!-----!-----! 120

L C P F G E V F N A T R F A S V Y A W N
CTGTGCCCTTCGGCGAGGTGTTCACGCCACCAGATTGCCAGCGGTACGCCTGGAAC
121 -----!-----!-----!-----!-----!-----! 180

R K R I S N C V A D Y S V L Y N S A S F
AGGAAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGTCTACAACAGCGCCAGCTTC
181 -----!-----!-----!-----!-----!-----! 240

S T F K C Y G V S P T K L N D L C F T N
AGCACCTTCAAGTGTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAAC
241 -----!-----!-----!-----!-----!-----! 300

V Y A D S F V I R G D E V R Q I A P G Q
GTGTACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAG
301 -----!-----!-----!-----!-----!-----! 360

T G K I A D Y N Y K L P D D F T G C V I
ACCGGCAAGATCGCCGACTACAACTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATC
361 -----!-----!-----!-----!-----!-----! 420

A W N S N N L D S K V G G N Y N Y L Y R
GCGTGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTCTACAGA
421 -----!-----!-----!-----!-----!-----! 480

L F R K S N L K P F E R D I S T E I Y Q
CTGTTCAAGAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAG
481 -----!-----!-----!-----!-----!-----! 540

A G S T P C N G V E G F N C Y F P L Q S
GCCGGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGC
541 -----!-----!-----!-----!-----!-----! 600

Y G F Q P T N G V G Y Q P Y R V V V L S
TACGGCTTCCAGCCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGC
601 -----!-----!-----!-----!-----!-----! 660

F E L L H A P A T V C G P K K S T N L V
TTCGAGCTGCTGCAGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACAATCTGGTG
661 -----!-----!-----!-----!-----!-----! 720

K N K C V N F G S G Y I P E A P R D G Q
AAGAACAAGTGCCTGAACCTCGGCAGCGGCTACATCCCCGAGGCCCCAGAGACGGCCAG
721 -----!-----!-----!-----!-----!-----! 780

A Y V R K D G E W V L L S T F L * **XhoI**
GCCTACGTGAGAAAGGACGGCGAGTGGGTGCTGCTGTCCACCTTCCTGTGATGACTCGAG
781 -----!-----!-----!-----!-----!-----! 840

B: Murine IgK Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 84)

HindIII M E T D T L L L W V L L L W V P
AAGCTTGGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTATTGTGGGTTCCTCC
1 -----!-----!-----!-----!-----!-----! 60

G S T G S D N G P Q N Q R N A P R I T F
GGTTCAACCGGCAGCGACAACGGCCCCCAGAACAGAGAAACGCCCCAGAAATCACCTTC
61 -----!-----!-----!-----!-----!-----! 120

Figure 3 continued

G G P S D S T G S N Q N G E R S G A R S
GGCGGCCCCAGCGACAGCACCGGCAGCAACCAGAACGGCGAGAGAAGCGGCCAGAAAGC
121 -----!-----!-----!-----!-----!-----! 180

K Q R R P Q G L P N N T A S W F T A L T
AAGCAGAGAAGACCCAGGGCTGCCCCAACACACCGCCAGCTGGTTACCGCCCTGACC
181 -----!-----!-----!-----!-----!-----! 240

Q H G K E D L K F P R G Q G V P I N T N
CAGCACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGCCCATCAACACCAAC
241 -----!-----!-----!-----!-----!-----! 300

S S P D D Q I G Y Y R R A T R R I R G G
AGCAGCCCCGACGACCATGCGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGC
301 -----!-----!-----!-----!-----!-----! 360

D G K M K D L S P R W Y F Y Y L G T G P
GACGGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCC
361 -----!-----!-----!-----!-----!-----! 420

E A G L P Y G A N K D G I I W V A T E G
GAGCCCCGCCCTGCCCTACGGGCCCAACAAGCAGGCATCATCTGGGTGCCACCGAGGGC
421 -----!-----!-----!-----!-----!-----! 480

A L N T P K D H I G T R N P A N N A A I
GCCCTGAACACCCCAAGGACCACATCGGCACCAGAAACCCCGCAACAACGCCGCCATC
481 -----!-----!-----!-----!-----!-----! 540

V L Q L P Q G T T L P K G F Y A E G S R
GTGCTCCAGTGGCCCCAGGGCACCCCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGA
541 -----!-----!-----!-----!-----!-----! 600

G G S Q A S S R S S S R S R N S S R N S
GGCGGCAGCCAGGCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGC
601 -----!-----!-----!-----!-----!-----! 660

T P G S S R G T S P A R M A G N G G D A
ACCCCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCT
661 -----!-----!-----!-----!-----!-----! 720

A L A L L L L D R L N Q L E S K M S G K
GCCCTGSCCTGTGCTGCTGGACAGACTGAACAGCTGGAGAGCAAGATGAGCGGCAAG
721 -----!-----!-----!-----!-----!-----! 780

G Q Q Q Q G Q T V T K K S A A E A S K K
GGCCAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCGGAGGCCAGCAAGAAG
781 -----!-----!-----!-----!-----!-----! 840

P R Q K R T A T K A Y N V T Q A F G R R
CCCAGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGA
841 -----!-----!-----!-----!-----!-----! 900

G P E Q T Q G N F G D Q E L I R Q G T D
GGCCCCGAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCGAC
901 -----!-----!-----!-----!-----!-----! 960

Y K H W P Q I A Q F A P S A S A F F G M
TACAAGCACTGGCCCCAGATCGCCAGTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATG
961 -----!-----!-----!-----!-----!-----! 1020

S R I G M E V T P S G T W L T Y T G A I
AGCAGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGGCGCCATC
1021 -----!-----!-----!-----!-----!-----! 1080

K L D D K D P N F K D Q V I L L N K H I
AAGCTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATC
1081 -----!-----!-----!-----!-----!-----! 1140

Figure 3 continued

D A Y K T F P P T E P K K D K K K K A D
GACGCCTACAAGACCTTCCCCCCACCGAGCCCAAGAGGACAAGAAGAAGAAGGCCGAC
1141 -----!-----!-----!-----!-----!-----! 1200

E T Q A L P Q R Q K K Q Q T V T L L P A
GAGACCCAGGCCCTGCCCGAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

A D L D D F S K Q L Q Q S M S S A D S T
GCCGACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACC
1261 -----!-----!-----!-----!-----!-----! 1320

Q A E P K S C D K T H T C P P C P A P E
CAGGCCGAGCCCAAATCGTGCGATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAG
1321 -----!-----!-----!-----!-----!-----! 1380

L L G G P S V F L F P P K P K D T L M I
TTGCTGGGTGGACCGAGCGTGTCTGTGTTTTCCCAAGCCCAAGGACACCTGATGATC
1381 -----!-----!-----!-----!-----!-----! 1440

S R T P E V T C V V V D V S H E D P E V
AGCAGAACCCCGAGCTGACCTGCCGTGGTGGACCTGAGCCACGAGACCCCGAGGTG
1441 -----!-----!-----!-----!-----!-----! 1500

K F N W Y V D G V E V H N A K T K P R E
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAGAGAG
1501 -----!-----!-----!-----!-----!-----! 1560

E Q Y N S T Y R V V S V L T V L H Q D W
GAGCAGTACAAACAGCACCTACAGAGTTGTGTCCTGCTGACCGTGTGCACACGAGACTGG
1561 -----!-----!-----!-----!-----!-----! 1620

L N G K E Y K C K V S N K A L P A P I E
CTGAACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGUCCGTGCCCGCCCCATCGAG
1621 -----!-----!-----!-----!-----!-----! 1680

K T I S K A K G Q P R E P Q V Y T L P P
AAGACCATCAGCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTGTACACCTGCCCCC
1681 -----!-----!-----!-----!-----!-----! 1740

S R D E L T K N Q V S L T C L V K G F Y
AGCAGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTGAAGGGCTTCTAC
1741 -----!-----!-----!-----!-----!-----! 1800

P S D I A V E W E S N G Q P E N N Y K T
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACCTACAAGACC
1801 -----!-----!-----!-----!-----!-----! 1860

T P P V L D S D G S F F L Y S K L T V D
ACCCCCCGCTGCTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGAC
1861 -----!-----!-----!-----!-----!-----! 1920

K S R W Q Q G N V F S C S V M H E A L H
AAGAGCAGATGGCAGCAGGGCAACGTGTTCTCTTGACGCTGATGCACGAGGCCCTGCAC
1921 -----!-----!-----!-----!-----!-----! 1980

N H Y T Q K S L S L S P G K *
AACCACCTACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGA
1981 -----!-----!-----!-----!-----!-----! 2040

PstI
ATTGCGCCTTAAGGGCTAATTC**TGCAG**
2041 -----!-----!-----! 2067

Figure 4: Sequence of pVAXDCSN3; SN3

A: Murine IgK Leader + Spike Glycoprotein (AA 319-541) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 85)

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BamHI      M E T D T L L L W V L L L W V P
GGATCCGGCACCATTGGAGACTGACACGCTCTTGCTTTGGGTGCTGTTATTGTGGGTTCCT
1  -----!-----!-----!-----!-----!-----! 60

      G S T G R V Q P T E S I V R F P N I T N
GGTTCAACCGGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAC
61 -----!-----!-----!-----!-----!-----! 120

      L C P F G E V F N A T R F A S V Y A W N
CTGTGCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCCAGCGGTACGCCTGGAAC
121 -----!-----!-----!-----!-----!-----! 180

      R K R I S N C V A D Y S V L Y N S A S F
AGGAAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTC
181 -----!-----!-----!-----!-----!-----! 240

      S T F K C Y G V S P T K L N D L C F T N
AGCACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGTGAACGACCTGTGCTTCACCAAC
241 -----!-----!-----!-----!-----!-----! 300

      V Y A D S F V I R G D E V R Q I A P G Q
GTGTACSCCGACAGCTTCGTGATCAGAGGCGACGAGTGAGACAGATCGCCCCCGGCCAG
301 -----!-----!-----!-----!-----!-----! 360

      T G K I A D Y N Y K L P D D F T G C V I
ACCGGCAAGATCGCGACTACAAC TACAAGCTGCCGACGACTTCACCGGCTGCGTGATC
361 -----!-----!-----!-----!-----!-----! 420

      A W N S N N L D S K V G G N Y N Y L Y R
GCGTGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAAC TACCTCTACAGA
421 -----!-----!-----!-----!-----!-----! 480

      L F R K S N L K P F E R D I S T E I Y Q
CTGTTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCAGAGATCTACCAG
481 -----!-----!-----!-----!-----!-----! 540

      A G S T P C N G V E G F N C Y F P L Q S
GCGGCGAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGC
541 -----!-----!-----!-----!-----!-----! 600

      Y G F Q P T N G V G Y Q P Y R V V V L S
TACGGCTTCCAGCCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTCTGAGC
601 -----!-----!-----!-----!-----!-----! 660

      F E L L H A P A T V C G P K K S T N L V
TTCGAGTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTG
661 -----!-----!-----!-----!-----!-----! 720

      K N K C V N F E P K S C D K T H T C P P
AAGAACAAGTGGTGAAC TCGAGCCCAAATCGTGCGATAAAACGCATACGTGCCCCCCC
721 -----!-----!-----!-----!-----!-----! 780

      C P A P E L L G G P S V F L F P P K P K
TGTCAGCCCCAGAGTTGCTGGGTGGACCGAGCGTGTTCTGTTCCTGTTCCTGTTCCTGTTC
781 -----!-----!-----!-----!-----!-----! 840

      D T L M I S R T P E V T C V V V D V S H
GACACCTGATGATCAGCAGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCAC
841 -----!-----!-----!-----!-----!-----! 900

      E D P E V K F N W Y V D G V E V H N A K
GAGGACCCCGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAG
901 -----!-----!-----!-----!-----!-----! 960
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Figure 4 continued

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T K P R E E Q Y N S T Y R V V S V L T V
ACCAAGCCCAGAGAGGAGCAGTACAACAGCACCTACAGAGTTGTGTCCTGCTGACCCGTG
961 -----!-----!-----!-----!-----!-----! 1020

L H Q D W L N G K E Y K C K V S N K A L
CTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTG
1021 -----!-----!-----!-----!-----!-----! 1080

P A P I E K T I S K A K G Q P R E P Q V
CCCGCCCCATCGAGAAGACCATCAGCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTG
1081 -----!-----!-----!-----!-----!-----! 1140

Y T L P P S R D E L T K N Q V S L T C L
TACACCTTGCCCCCAGCAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCGCTG
1141 -----!-----!-----!-----!-----!-----! 1200

V K G F Y P S D I A V E W E S N G Q P E
GTGAAGGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAG
1201 -----!-----!-----!-----!-----!-----! 1260

N N Y K T T P P V L D S D G S F F L Y S
AACAACTACAAGACCACCCCCCGTCTGACAGCCACGGCAGCTTCTTCTCTACAGC
1261 -----!-----!-----!-----!-----!-----! 1320

K L T V D K S R W Q Q G N V F S C S V M
AAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCTCTTGACGCGTGATG
1321 -----!-----!-----!-----!-----!-----! 1380

H E A L H N H Y T Q K S L S L S P G K *
CAGGAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGA
1381 -----!-----!-----!-----!-----!-----! 1440

XhoI
TGACTCGAG
1441 ----- 1449
```

B: Murine IgK Leader + Nucleoprotein (AA 2-419) (SEQ ID NO: 86)

```
HindIII M E T D T L L L W V L L L W V P
AAGCTTGCCACCATGGAGACTGACACGCTCTTGCTTGGGTGCTGTATTGTGGTTCCC
1 -----!-----!-----!-----!-----!-----! 60

G S T G S D N G P Q N Q R N A P R I T F
GGTTCAACCGGCAGCGACAACGGCCCCCAGAACAGAGAAACGCCCCAGAAATCACCTTC
61 -----!-----!-----!-----!-----!-----! 120

G G P S D S T G S N Q N G E R S G A R S
GGCGGCCCCAGCGACAGCACCGGCAGCAACCAGAACCGCGAGAGAAGCGGCGCCAGAACG
121 -----!-----!-----!-----!-----!-----! 180

K Q R R P Q G L P N N T A S W F T A L T
AAGCAGAGAAGACCCAGGGCCTGCCAACAAACCGCCAGCTGGTTCACCGCCCTGACC
181 -----!-----!-----!-----!-----!-----! 240

Q H G K E D L K F P R G Q G V P I N T N
CAGCACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGCCCATCAACACCAAC
241 -----!-----!-----!-----!-----!-----! 300

S S P D D Q I G Y Y R R A T R R I R G G
AGCAGCCCCGACGACCATCGGCTACTACAGAAGAGCCACAGAGAATCAGAGGCGGC
301 -----!-----!-----!-----!-----!-----! 360

D G K M K D L S P R W Y F Y Y L G T G P
GACGGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGCCCC
361 -----!-----!-----!-----!-----!-----! 420
```

Figure 4 continued

E A G L P Y G A N K D G I I W V A T E G
GAGGCCGECCTGCCCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGC
421 -----!-----!-----!-----!-----!-----! 480

A L N T P K D H I G T R N P A N N A A I
GCCCTGAACACCCCAAGGACACATCGGCACCAGAAACCCGCCAACGCGCCCATC
481 -----!-----!-----!-----!-----!-----! 540

V L Q L P Q G T T L P K G F Y A E G S R
GTGCTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGA
541 -----!-----!-----!-----!-----!-----! 600

G G S Q A S S R S S S R S R N S S R N S
GGCGGCAGCCAGGCCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGC
601 -----!-----!-----!-----!-----!-----! 660

T P G S S R G T S P A R M A G N G G D A
ACCCCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCT
661 -----!-----!-----!-----!-----!-----! 720

A L A L L L L D R L N Q L E S K M S G K
GCCCTGCGCCCTGCTGCTGCTGACAGACTGAACCAGCTGGAGACCAAGATGACCGCAAG
721 -----!-----!-----!-----!-----!-----! 780

G Q Q Q Q G Q T V T K K S A A E A S K K
GGCCAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCGAGGCCAGCAAGAAG
781 -----!-----!-----!-----!-----!-----! 840

P R Q K R T A T K A Y N V T Q A F G R R
CCGAGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGA
841 -----!-----!-----!-----!-----!-----! 900

G P E Q T Q G N F G D Q E L I R Q G T D
GGCCCCGAGCAGACCCAGGGCAACTTCGGCGACCCAGGAGCTGATCAGACAGGGCACCGAC
901 -----!-----!-----!-----!-----!-----! 960

Y K H W P Q I A Q F A P S A S A F F G M
TACAAGCACTGGCCCCAGATCGCCCAAGTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATG
961 -----!-----!-----!-----!-----!-----! 1020

S R I G M E V T P S G T W L T Y T G A I
AGCAGAACTCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGGCGCCATC
1021 -----!-----!-----!-----!-----!-----! 1080

K L D D K D P N F K D Q V I L L N K H I
AAGCTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATC
1081 -----!-----!-----!-----!-----!-----! 1140

D A Y K T F P P T E P K K D K K K K A D
GACGCCTACAAGACCTTCCCCCACCAGGCCCAAGAAGGACAAGAAGAAGAAGGCCGAC
1141 -----!-----!-----!-----!-----!-----! 1200

E T Q A L P Q R Q K K Q Q T V T L L P A
GAGACCCAGGCCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCCGC
1201 -----!-----!-----!-----!-----!-----! 1260

A D L D D F S K Q L Q Q S M S S A D S T
GCGGACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACC
1261 -----!-----!-----!-----!-----!-----! 1320

Q A * *Pst*I
CAGGCCTGATGATCTAAAGGGCGAATTCGCCCTTAAGGGCTAATTCTGCAG
1321 -----!-----!-----!-----!-----!-----!- 1371

Figure 5: Sequence of pVAXDCSN4; SN4

A: Murine IgK Leader + Spike Glycoprotein (AA 319-541) (SEQ ID NO: 87)

BamHI M E T D T L L L W V L L L W V P
GGATCCGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTTATTGTGGGTTCCTC
1 -----!-----!-----!-----!-----!-----!-----! 60

G S T G R V Q P T E S I V R F P N I T N
GGTTCAACCGGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAAC
61 -----!-----!-----!-----!-----!-----!-----! 120

L C P F G E V F N A T R F A S V Y A W N
CTGTGCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCCAGCGTGATACGCTGGAAC
121 -----!-----!-----!-----!-----!-----!-----! 180

R K R I S N C V A D Y S V L Y N S A S F
AGGAAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGTCTACAACAGCGCCAGCTTC
181 -----!-----!-----!-----!-----!-----!-----! 240

S T F K C Y G V S P T K L N D L C F T N
AGCACCTTCAAGTGTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAAC
241 -----!-----!-----!-----!-----!-----!-----! 300

V Y A D S F V I R G D E V R Q I A P G Q
GTGTACGCCGACAGCTTCGTGATCAGAGCGCAGAGGTGAGACAGATCGCCCCGGCCAG
301 -----!-----!-----!-----!-----!-----!-----! 360

T G K I A D Y N Y K L P D D F T G C V I
ACCGGCAAGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATC
361 -----!-----!-----!-----!-----!-----!-----! 420

A W N S N N L D S K V G G N Y N Y L Y R
GCGTGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTACAGA
421 -----!-----!-----!-----!-----!-----!-----! 480

L F R K S N L K P F E R D I S T E I Y Q
CTGTTCAAGAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCAGAGATCTACCA
481 -----!-----!-----!-----!-----!-----!-----! 540

A G S T P C N G V E G F N C Y F P L Q S
GCCGGCAGACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGC
541 -----!-----!-----!-----!-----!-----!-----! 600

Y G F Q P T N G V G Y Q P Y R V V V L S
TACGGCTTCCAGCCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGC
601 -----!-----!-----!-----!-----!-----!-----! 660

F E L L H A P A T V C G P K K S T N L V
TTCGAGCTGTGCAGCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTG
661 -----!-----!-----!-----!-----!-----!-----! 720

K N K C V N F * **Xho**I
AAGAACAAGTGCCTGAACCTCTGATGACTCGAG
721 -----!-----!-----!-----!-----!-----!-----! 753

B: Murine IgK Leader + Nucleoprotein (AA 2-419) (SEQ ID NO: 88)

HindIII M E T D T L L L W V L L L W V P
AAGCTTGCCACCATGGAGACTGACACGCTCTTGCTTTGGGTGCTGTTATTGTGGGTTCCTC
1 -----!-----!-----!-----!-----!-----!-----! 60

G S T G S D N G P Q N Q R N A P R I T F
GGTTCAACCGGCAGCGACAACGCCCCAGAACAGAGAAACGCCCCAGAAATCACCTTC
61 -----!-----!-----!-----!-----!-----!-----! 120

Figure 5 continued

G G P S D S T G S N Q N G E R S G A R S
GGCGGCCCCAGCGACAGCACCGGCAGCAACCGGCGAGAGAAGCGCGCCAGAAGC
121 -----!-----!-----!-----!-----!-----! 180

K Q R R P Q G L P N N T A S W F T A L T
AAGCAGAGAAGACCCAGGGCCTGCCCAACAACCGGCCAGCTGGTTCACCGCCCTGACC
181 -----!-----!-----!-----!-----!-----! 240

Q H G K E D L K F P R G Q G V P I N T N
CAGCACGGCAAGGAGGACCTGAAGTTCCTCAGAGGCCAGGGCGTGCCCATCAACACCAAC
241 -----!-----!-----!-----!-----!-----! 300

S S P D D Q I G Y Y R R A T R R I R G G
AGCAGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGC
301 -----!-----!-----!-----!-----!-----! 360

D G K M K D L S P R W Y F Y Y L G T G P
GAGGCCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCC
361 -----!-----!-----!-----!-----!-----! 420

E A C L P Y G A N K D G I I W V A T E G
GAGGCCGGCCTGCCCCACGCGGCCAACAGGACGGCATCATCTGGGTGGCCACCGAGGGC
421 -----!-----!-----!-----!-----!-----! 480

A L N T P K D H I G T R N P A N N A A I
GCCCTGAACACCCCCAAGGACCACATCGGCACAGAAACCCCGCCAACAACGCCGCCATC
481 -----!-----!-----!-----!-----!-----! 540

V L Q L P Q G T T L P K G F Y A E G S R
GTGCTCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGA
541 -----!-----!-----!-----!-----!-----! 600

G G S Q A S S R S S S R S R N S S R N S
GGCGGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGC
601 -----!-----!-----!-----!-----!-----! 660

T P G S S R G T S P A R M A G N G G D A
ACCCCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCT
661 -----!-----!-----!-----!-----!-----! 720

A L A L L L L D R L N Q L E S K M S G K
GCCCTGCCCCGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAG
721 -----!-----!-----!-----!-----!-----! 780

G Q Q Q Q G Q T V T K K S A A E A S K K
GGCCAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCCGAGGCCAGCAAGAAG
781 -----!-----!-----!-----!-----!-----! 840

P R Q K R T A T K A Y N V T Q A F G R R
CCCAGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGA
841 -----!-----!-----!-----!-----!-----! 900

G P E Q T Q G N F G D Q E L I R Q G T D
GGCCCCGAGCAGACCCAGGGCAACTTCGGCGACCGAGGCTGATCAGACAGGGCACCGAC
901 -----!-----!-----!-----!-----!-----! 960

Y K H W P Q I A Q F A P S A S A F F G M
TACAAGCACTGGCCCCAGATCGCCAGTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATG
961 -----!-----!-----!-----!-----!-----! 1020

S R I G M E V T P S G T W L T Y T G A I
AGCAGAATCGGCATGGAGGTGACCCCGAGCGGCACCTGGCTGACCTACACGGCGGCCATC
1021 -----!-----!-----!-----!-----!-----! 1080

K L D D K D P N F K D Q V I L L N K H I
AAGCTGACGACAAGGACCCCAACTCAAGGATCAGGTGATCCTGCTGAACAAGCACATC
1081 -----!-----!-----!-----!-----!-----! 1140

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Figure 5 continued

```

      D A Y K T F P P T E P K K D K K K K A D
1141 GACGCCTACAAGACCTTCCCCCCCACCGAGCCCAAGAAGGACAAGAAGAAGAGCCGAC
-----!-----!-----!-----!-----!-----! 1200

      E T Q A L P Q R Q K K Q Q T V T L L P A
1201 GAGACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCC
-----!-----!-----!-----!-----!-----! 1260

      A D L D D F S K Q L Q Q S M S S A D S T
1261 GCCGACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACC
-----!-----!-----!-----!-----!-----! 1320

      Q A *
1321 CAGGCCTGATGATCTAAAGGGCGAATTCGCCCTTAAGGGCTAATTCTGCAG
-----!-----!-----!-----!-----!-----!- 1371

```

Figure 6: Sequence of pVAXDCSN5; SN5

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) (SEQ ID NO: 89)

```

      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I T N L
61 GCACACAGCAGATGCAGCCCACCGAGAGCATCGTGAGATCCCCAACATCACCACCTG
-----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
121 TGCCCTTCGGCGAGGTGTTCAACGCCACCAGATTCGCCAGCGTGACGCCTGGAACAGG
-----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
181 AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
-----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F T N V
241 ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
-----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
301 TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCCGGCCAGACC
-----!-----!-----!-----!-----!-----! 360

      G K I A D Y N Y K L P D D F T G C V I A
361 GGCAAGATCGCCGACTACAACATAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
-----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
421 TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTACAGACTG
-----!-----!-----!-----!-----!-----! 480

      F R K S N L K P F E R D I S T E I Y Q A
481 TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCAGATCTACCAGGCC
-----!-----!-----!-----!-----!-----! 540

      G S T P C N G V E G F N C Y F P L Q S Y
541 GGCAGCACCCTTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
-----!-----!-----!-----!-----!-----! 600

      G F Q P T N G V G Y Q P Y R V V V L S F
601 GGCTTCCAGCCCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGCTTC
-----!-----!-----!-----!-----!-----! 660

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Figure 6 continued

```
      E L L H A P A T V C G P K K S T N L V K
      GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

      N K C V N F *      XhoI
      AACAAGTGGGTGAACCTTCTGATGACTCGAG
721 -----!-----!-----! 750
```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 90)

```
      HindIII      M D W I W R I L F L V G A A T G
      AAGCTTGCCACCATGGACTGGATTTGGAGAATCCTCTTCCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
      GCACACAGCAGCGACAACGGCCCCCAGAACAGAGAAACGCCCCAGAAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
      GGCCCCAGCGACAGCACCGGCAGCAACAGAACGGCCGAGAGAAGCGGCGCCAGAAAGCAAG
121 -----!-----!-----!-----!-----!-----! 180

      Q R R P Q G L P N N T A S W F T A L T Q
      CAGAGAAGACCCAGGGCCTGCCAACACACCGCCAGCTGGTTCACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

      H G K E D L K F P R G Q G V P I N T N S
      CACGGCAAGGAGGACCTGAAGTTCCCCAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

      S P D D Q I G Y Y R R A T R R I R G G D
      AGCCCCGACGACCATCGGCTACTACAGAAGAGCCACCCAGAAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----! 360

      G K M K D L S P R W Y F Y Y L G T G P E
      GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCGACGGCCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

      A G L P Y G A N K D G I I W V A T E G A
      GCGGCGCTGCCCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

      L N T P K D H I G T R N P A N N A A I V
      CTGAACACCCCCAAGGACCACATCGGCACCCAGAAACCCCGCCAACAACGCCGCGCATCTG
481 -----!-----!-----!-----!-----!-----! 540

      L Q I P Q G G T T L P K G F Y A E G S R G
      CTCCAGCTGCCCGAGGGCACCCCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

      G S Q A S S R S S S R S R N S S R N S T
      GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

      P G S S R G T S P A R M A G N G G D A A
      CCTGGAAGCTCAAGGGGACCTCTCCTGCGCGGATGGCTGCTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

      L A L L L L D R L N Q L E S K M S G K G
      CTGGCCCTGTGTGCTGGACAGACTGAACCAAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

      Q Q Q Q G Q T V T K K S A A E A S K K P
      CAGCAGCAGAGGGCCAGACTGTGACCAAAAAAGCGCGCGGAGGCCAGCAAGAAGGCC
781 -----!-----!-----!-----!-----!-----! 840
```

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Figure 6 continued

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCCAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCAGCTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I C M E V T P S G T W L T Y T G A I K
AGAATCGCATGGAGGTGACCCCCAGCGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCACCAGCCCAAGAAGCACAGAAGAAGAGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAGCAGCAGACAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAAAATCGTGCGATAAAACGCATACGTGCCCCCTGTGCCAGCCCAAGATTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTCTGTTCCTGTTCCTCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGGAGGTGACCTGCGTGGTGGTGGAGCTGAGCCACGAGGACCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H N A K T K P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGATTGTGTCCGTGCTGACCGTGTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K A K G Q P R E P Q V Y T L P P S
ACCATCAGCAAGGCCAAGGCCAGCCAGAGAGCCCCAGGTGTACACCCTGCCCGCCAGC
1681 -----!-----!-----!-----!-----!-----! 1740

R D E L T K N Q V S L T C L V K G F Y P
AGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTGAAGGGCTTCTACCCC
1741 -----!-----!-----!-----!-----!-----! 1800

S D I A V E W E S N G Q P E N N Y K T T
AGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

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Figure 6 continued

```

      P P V L D S D G S F F L Y S K L T V D K
      CCCCCGTGCTGGACAGCGACGGCAGCTTCTTCCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920
      S R W Q Q G N V F S C S V M H E A L H N
      AGCAGATGGCAGCAGGGCAACGTGTTCTTTCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980
      H Y T Q K S L S L S P G K *
      CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040
              PstI
      CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!----- 2064

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Figure 7: Sequence of pVAXDCSN6; SN6

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) + GS linker + Fibrin Trimer Motif (SEQ ID NO: 91)

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      BamHI          M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60
      A H S R V Q P T E S I V R F P N I T N L
      GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATCCCCAACATCACCAACCTG
61 -----!-----!-----!-----!-----!-----! 120
      C P F G E V F N A T R F A S V Y A W N R
      TGCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCCAGCGTGACGCCCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180
      K R I S N C V A D Y S V L Y N S A S F S
      AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240
      T F K C Y G V S P T K L N D L C F T N V
      ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTACCAACCTG
241 -----!-----!-----!-----!-----!-----! 300
      Y A D S F V I R G D E V R Q I A P G Q T
      TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360
      G K I A D Y N Y K L P D D F T G C V I A
      GGCAAGATCGCCGACTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420
      W N S N N L D S K V G G N Y N Y L Y R L
      TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480
      F R K S N L K P F E R D I S T E I Y Q A
      TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACAGGCC
481 -----!-----!-----!-----!-----!-----! 540
      G S T P C N G V E G F N C Y F P L Q S Y
      GGCGACACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600
      G F Q P T N G V G Y Q P Y R V V V L S F
      GGCTTCAGCCACCAACGGCGTGGGCTACCGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660
      E L L H A P A T V C G P K K S T N L V K
      GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

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Figure 7 continued

```
      N K C V N F G S G Y I P E A P R D G Q A
AACAAAGTGCCTGAACTTCGGCAGCGGCTACATCCCCGAGGCCCCAGAGACGGCCAGGCC
721 -----!-----!-----!-----!-----!-----!-----! 780

      Y V R K D G E W V L L S T F L *      XhoI
TACGTGAGAAAGGACGGCGAGTGGGTGCTGCTGTCCACCTTCTGTGATGACTCGAG
781 -----!-----!-----!-----!-----!-----!-----! 837
```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuIgG1 Hinge-CH2-CH3 (SEQ ID NO: 90)

```
      HindIII      M D W I W R I L F L V G A A T G
AAGCTTGCCACCATGGACTGGATTTGGAGAATCCTCTTCCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCAGAACGAGAAACGCCCCAGAAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCAGCAACGAGAACGGCGAGAGAAGCGGCGCCAGAAAGCAAG
121 -----!-----!-----!-----!-----!-----!-----! 180

      Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCAACACACCGCCAGCTGGTTACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----!-----! 240

      H G K E D L K F P R G Q G V P I N T N S
CAGGGCAAGGAGGACCTGAAGTTCCCCAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----!-----! 300

      S P E D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----!-----! 360

      G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGGAG
361 -----!-----!-----!-----!-----!-----!-----! 420

      A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCGCTACGGCGCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----!-----! 480

      L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCAAGGACCACATCGGCACCAGAAACCCGCAACAACGCCGCCATCGTG
481 -----!-----!-----!-----!-----!-----!-----! 540

      L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCCCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----!-----! 600

      G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----!-----! 660

      P G S S R G T S P A R M A G N G G D A A
CCTGGAACCTCAAGGGGACCTCTCCTGCGCGGATGGCTGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----!-----! 720

      L A L L L L L D R L N Q L E S K M S G K G
CTGGCCCTGTGTGCTGGACAGACTGAACCAAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----!-----! 780

      Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGAGGGCCAGACTGTGACCAAAAAAGCGCCCGAGGCCAGCAAGAAGGCC
781 -----!-----!-----!-----!-----!-----!-----! 840
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Figure 7 continued

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCCAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCAGCTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I C M E V T P S G T W L T Y T G A I K
AGAATCGCATGGAGGTGACCCCGCGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCACCAGCCCAAGAAGCACAGAAGAAGAGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAGCAGCAGACAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAAAATCGTGCGATAAAACGCATACGTGCCCCCTGTGCCAGCCCAAGATTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTCTGTTCCTGTTCCTCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGGAGGTGACCTGCGTGGTGGTGGAGCTGAGCCACGAGGACCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H N A K T K P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGATTGTGTCCGTGCTGACCGTGTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K A K G Q P R E P Q V Y T L P P S
ACCATCAGCAAGGCCAAGGCCAGCCAGAGAGCCCCAGGTGTACACCCTGCCCGCCAGC
1681 -----!-----!-----!-----!-----!-----! 1740

R D E L T K N Q V S L T C L V K G F Y P
AGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTGAAGGGCTTCTACCCC
1741 -----!-----!-----!-----!-----!-----! 1800

S D I A V E W E S N G Q P E N N Y K T T
AGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

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Figure 7 continued

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      P P V L D S D G S F F L Y S K L T V D K
      CCCCCGTGGACAGCGACGGCAGCTTCTTCCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920
      S R W Q Q G N V F S C S V M H E A L H N
      AGCAGATGGCAGCAGGGCAACGTGTTCTTTCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980
      H Y T Q K S L S L S P G K *
      CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040
              PstI
      CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!----- 2064

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Figure 8: Sequence of pVAXDCSN7; SN7

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 92)

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      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTTGGAGAATCCTCTTCCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60
      A H S R V Q P T E S I V R F P N I T N L
      GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAACCTG
61  -----!-----!-----!-----!-----!-----! 120
      C P F G E V F N A T R F A S V Y A W N R
      TGCCCCCTTCGGCGAGGTGTTCAACGCCACCAGATTCCGCCAGCGTGACGCCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180
      K R I S N C V A D Y S V L Y N S A S F S
      AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240
      T F K C Y G V S P T K L N D L C F T N V
      ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300
      Y A D S F V I R G D E V R Q I A P G Q T
      TACGCCACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360
      G K I A D Y N Y K L P D D F T G C V I A
      GGCAAGATCGCCGACTACAATAACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420
      W N S N N L D S K V G G N Y N Y L Y R L
      TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAATACTCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480
      F R K S N L K P F E R D I S T E I Y Q A
      TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540
      G S T P C N G V E G F N C Y F P L Q S Y
      GGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600
      G F Q P T N G V G Y Q P Y R V V V L S F
      GGCTTCAGCCCAACCAACGGCGTGGGCTACCAAGCCCTACAGAGTGGTGGTCCCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660
      E L L H A P A T V C G P K K S T N L V K
      GAGCTGCTGCACGCCCCCGCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

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Figure 8 continued

N K C V N F E P K S C D K T H T C P P C
AACAAAGTGCCTGAACTTCGAGCCCAAATCGTGCGATAAAACGCATACGTGCCCCCCTGT
721 -----!-----!-----!-----!-----!-----! 780

P A P E L L G G P S V F L F P P K P K D
CCAGCCCAGAGTTGCTGGGTGGACCGAGCGTGTCTGTTCCTGTTCCCCCAAGCCCAAGGAC
781 -----!-----!-----!-----!-----!-----! 840

T L M I S R T P E V T C V V V D V S H E
ACCCTGATGATCAGCAGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAG
841 -----!-----!-----!-----!-----!-----! 900

D P E V K F N W Y V D G V E V H N A K T
GACCCCGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACC
901 -----!-----!-----!-----!-----!-----! 960

K P R E E Q Y N S T Y R V V S V L T V L
AAGCCCGAGAGGAGCAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTG
961 -----!-----!-----!-----!-----!-----! 1020

H Q D W L N G K E Y K C K V S N K A L P
CACCAGGACTGGCTGAACGGCAAGGACTACAAGTCCAAGGTGACCAACAAGGCCCTGCCC
1021 -----!-----!-----!-----!-----!-----! 1080

A P I E K T I S K A K G Q P R E P Q V Y
GCCCCATCGAGAAGACCATCAGCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTGTAC
1081 -----!-----!-----!-----!-----!-----! 1140

T L P P S R D E L T K N Q V S L T C L V
ACCCTGCCCCCAGCAGAGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTG
1141 -----!-----!-----!-----!-----!-----! 1200

K G F Y P S D I A V E W E S N G Q P E N
AAGGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAAC
1201 -----!-----!-----!-----!-----!-----! 1260

N Y K T T P P V L D S D G S F F L Y S K
AATACAGACACCCCCCGTGTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAG
1261 -----!-----!-----!-----!-----!-----! 1320

L T V D K S R W Q Q G N V F S C S V M H
CTGACCTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCTTTCAGCGTGATGCAC
1321 -----!-----!-----!-----!-----!-----! 1380

E A L H N H Y T Q K S L S L S P G K *
GAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGA
1381 -----!-----!-----!-----!-----!-----! 1440

XhoI
CTCGAG
1441 ----- 1446

B: Human IgH Leader + Nucleoprotein (AA 2-419) (SEQ ID NO: 93)

HindIII M D W I W R I L F L V G A A T G
AAGCTTGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCAGAACGAGAAACGCCCCAGAAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCAGCAACGAGACGGCGAGAGAAGCGCGCCAGAGCAAG
121 -----!-----!-----!-----!-----!-----! 180

Figure 8 continued

Q R R P Q G L P N N T A S W F T A L T Q
181 CAGAGAAGACCCAGGGCCTGCCCAACAACACGCCAGCTGGTTCACCGCCCTGACCCAG 240
-----!-----!-----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
241 CACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCTGCCCATCAACACCAACAGC 300
-----!-----!-----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
301 AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC 360
-----!-----!-----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
361 GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGGAG 420
-----!-----!-----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
421 GCCGGCCTGCCCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGGCC 480
-----!-----!-----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
481 CTGAACACCCCAAGCACCATCGGCACCAGAAACCCGCCAACAACCGGCCCATCGTG 540
-----!-----!-----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
541 CTCCAGTGGCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC 600
-----!-----!-----!-----!-----!-----!-----! 600

G S Q A S S R S S S R S R N S S R N S T
601 GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC 660
-----!-----!-----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
661 CCTGGAAGCTCAAGGGGCACCTCTCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC 720
-----!-----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
721 CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAGGGC 780
-----!-----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
781 CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC 840
-----!-----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
841 AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC 900
-----!-----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
901 CCCGAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCGACTAC 960
-----!-----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
961 AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC 1020
-----!-----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
1021 AGAATCGGCATGGAGGTGACCCCGAGCGCACCTGGCTGACCTACACCGCGGCCATCAAG 1080
-----!-----!-----!-----!-----!-----!-----! 1080

L D E K D P N F K D Q V I L L N K H I D
1081 CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC 1140
-----!-----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
1141 GCCTACAAGACCTTCCCCCACCAGGCCAAGAAGGACAAGAAGAAGAAGGCCGACGAG 1200
-----!-----!-----!-----!-----!-----!-----! 1200

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Figure 8 continued

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      T Q A L P Q R Q K K Q Q T V T L L P A A
      ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

      D L D D F S K Q L Q Q S M S S A D S T Q
      GACCTGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

      A *
      GCCTGATGATCTAAAGGGCGAATTGCGCCCTTAAGGGCTAATTCTGCAG
1321 -----!-----!-----!-----!-----!-----! 1368

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Figure 9: Sequence of pVAXDCSN8; SN8

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) (SEQ ID NO: 89)

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      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I I' N L
      GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAACCTG
61 -----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
      TGCCCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCCAGCGTGACGCCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
      AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F T N V
      ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
      TACGCCACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360

      G K I A D Y N Y K L P D D F T G C V I A
      GGCAAGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
      TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480

      F R K S N L K P F E R D I S T E I Y Q A
      TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540

      G S T P C N G V E G F N C Y F P L Q S Y
      GGCAGCACCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600

      G F Q P T N G V G Y Q P Y R V V V L S F
      GGGTTCCAGCCACCAACGGCGTGGGCTACCGCCCTACAGAGTGGTGGTCCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660

      E L L H A P A T V C G P K K S T N L V K
      GAGCTGTGCAGCCCCCGCCACCCTGTGCGGCCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

      N K C V N F *      XhoI
      AACAAGTGGTGAACTTCTGATGACTCGAG
721 -----!-----!-----!-----!-----!-----! 750

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Figure 9 continued

B: Human IgH Leader + Nucleoprotein (AA 2-419) (SEQ ID NO: 93)

HindIII M D W I W R I L F L V G A A T G
AAGCTT GCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----! 60

A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCCACAACGGCCCCAGAACCAGAGAAACGCCCCAGAATCACCTTCGGC
61 -----!-----!-----!-----!-----! 120

G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCAGGAGCAACCAGAACGGCGAGAGAAGCGGCCAGAGCAAG
121 -----!-----!-----!-----!-----! 180

Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACACCGCCAGCTGGTTCACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGGCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCAGCAGCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGGAG
361 -----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCCCCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCAAGGACCACATCGGCACCAGAAACCCGCCAACAACGCCGCATCGTG
481 -----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----! 600

G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGGACAGACTGAACCAAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGAGGGCCAGACTGTGACCAAAAAAGCGCCGCCAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCGAGCAGACCCAGGGCAACTTCGGCGACCAAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----! 960

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Figure 9 continued

```

      K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCCCAGTTCGCCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

      R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

      L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

      A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCCACCGAGCCCAAGAAGGACAAGAAGAAGGCGGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

      T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

      D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGCATGAGCAGCGCCGACAGCACCAG
1261 -----!-----!-----!-----!-----!-----! 1320

      A *
GCCTGATGATCTAAAGGGCGAATTGCGCCCTTAAGGGCTAATTCTGCAG
1321 -----!-----!-----!-----!-----!-----! 1368

```

Figure 10: Sequence of pVAXDCSN9; SN9

A: Human IgH Leader + Spike Glycoprotein (AA 330—525) + GS linker + Fibrin v2 Trimer Motif (GTGGGSG)
(SEQ ID NO: 94)

```

      BamHI      M D W I W R I L F L V G A A T G
GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S P N I T N L C P F G E V F N A T R
GCACACAGCCCAACATCACCAATCTGTGCCCTTTCGGCGAGGTGTTCAACGCCACCAGA
61 -----!-----!-----!-----!-----!-----! 120

      F A S V Y A W N R K R I S N C V A D Y S
TTCGCTCTGTGTACGCTTGAACCGGAAGCGGATCAGCAATTGCGTGGCCGACTACAGC
121 -----!-----!-----!-----!-----!-----! 180

      V L Y N S A S F S T F K C Y G V S P T K
GTGCTGTACAACAGCGCCAGCTTCAGCACCTTCAAGTGCTACGGCGTGTCCCCTACCAAG
181 -----!-----!-----!-----!-----!-----! 240

      L N D L C F T N V Y A D S F V I R G D E
CTGAACGATCTGTGCTTCACCAACGTGTACGCGGACAGCTTCGTGATCAGAGGCGACGAA
241 -----!-----!-----!-----!-----!-----! 300

      V R Q I A P G Q T G K I A D Y N Y K L P
GTGCGGCGAGATTGCCCCTGGACAGACAGGCAAGATCGCCGATTACAACACAAGCTGCCC
301 -----!-----!-----!-----!-----!-----! 360

      D D F T G C V I A W N S N N L D S K V G
GACGACTTCACCGGCTGTGTGATTGCCTGGAACAGCAACAACCTGGACAGCAAAGTCGGC
361 -----!-----!-----!-----!-----!-----! 420

      G N Y N Y L Y R L F R K S N L K P F E R
GGCAACTACAACCTACCTGTACCGGCTGTTCGGGAAGTCCAACCTGAAGCCTTTCGAGCGG
421 -----!-----!-----!-----!-----!-----! 480

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```

D I S T E I Y Q A G S T P C N G V G E G F
GACATCAGCACCAGATCTATCAGGCCGGCAGCACCCCTTGCAATGGCGTGGAAAGGCTTC
481 -----!-----!-----!-----!-----!-----!-----! 540

N C Y F P L Q S Y G F Q P T N G V G Y Q
AACTGCTACTTCCCACCTCCAGTCTCCTACGGCTTCCAGCCTACAAACGGCGTGGGCTACCAAG
541 -----!-----!-----!-----!-----!-----!-----! 600

P Y R V V V L S F E L L H A P A T V C G
CCTTACAGAGTGGTGGTCTGAGCTTCGAGCTGCTGCATGCTCCTGCTACAGTGGTGGC
601 -----!-----!-----!-----!-----!-----!-----! 660

G C S C G G S G C G S G S G Y I P E A P
GGAGGTCTGGCGGAGGAAGCGGAGGCGGATCTGGCTCTGGATATATTCCCGAGGCTCCC
661 -----!-----!-----!-----!-----!-----!-----! 720

R D G Q A Y V R K D G E W V L L S T F L
AGAGATGGCCAGGCCTATGTTTGGAAAGGATGGCGAGTGGGTCTGCTGAGCACATTTC
721 -----!-----!-----!-----!-----!-----!-----! 780

G T G G G S G * XhoI
CGAACAGCCGCCGAAGCCGATGATCACTCGAG
781 -----!-----!-----!-----!-----!-----!-----! 813

```

HindIII M D W I W R I L F L V G A A T G
AAGCTTGCACCATGGACTGGATTGGAGAAATCCTCTCTGGTGGGAGCTGCCACAGGC

1 -----!-----!-----!-----!-----!-----!-----! 60

A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCGAGAACCAGAGAAACGGCCCCCAGAATCACCTTCGGC

61 -----!-----!-----!-----!-----!-----!-----! 120

G P S D S T T G S N Q N G E R S G A R S K
GGCCCCAGCGCAGCACCGGCAGCAACCGAGAACGGCGAGAGAAGCGGCCACAGAAGCAAG

121 -----!-----!-----!-----!-----!-----!-----! 180

Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCAACAAACACCGCCAGCTGGTTACCGCCCTGACCCAG

181 -----!-----!-----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGCCCATCAACACCAACAGC

241 -----!-----!-----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC

301 -----!-----!-----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGTACTTCTACTACCTGGGCACCGGCCCCGAG

361 -----!-----!-----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCGCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC

421 -----!-----!-----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACAGAAACCCGGCAACAACGGCGCCATCTGT

481 -----!-----!-----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTTGCCCCAAGGGCTTCTACGCGCAGGGCAGCAGAGGC

541 -----!-----!-----!-----!-----!-----!-----! 600

Figure 10 continued

G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCAGCCACCAAGGCTTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCCAGCAGACCCAGCGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCAGCTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCCCACCGAGCCCAAGAAGGACAAGAAGAAGAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGSGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCGCGCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAATTCGTGCGATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCTGTTCCTGTTCCCCCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H N A K T K P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

Figure 10 continued

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      N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

      T I S K A K G Q P R E P Q V Y T L P P S
ACCATCAGCAAGGCCAAGGGCCAGCCAGAGAGCCCCAGGTGTACACCCTGCCCCCAGC
1681 -----!-----!-----!-----!-----!-----! 1740

      R D E L T K N Q V S L T C L V K G F Y P
AGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTGAAGGGCTTCTACCCC
1741 -----!-----!-----!-----!-----!-----! 1800

      S D I A V E W E S N G Q P E N N Y K T T
AGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCGAGAACACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

      P P V L D S D G S F F L Y S K L T V D K
CCCCCTGTGCTGGACAGCGACGGCAGCTTCTTCCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

      S R W Q Q G N V F S C S V M H E A L H N
AGCAGATCGCAGCAGCGCAACGTCTTCTCTTGCAGCCTGATCCAGCGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040

      PstI
CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----!-----! 2064

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Figure 11: Sequence of pVAXDCSN10; SN10

A: Human IgH Leader + Spike Glycoprotein (AA 330—525) + GS linker + Disulphide bridge motif (SEQ ID NO: 95)

```

      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGCACTGCATTTCGAGAATCCTCTTCCTGCTGGCAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S P N I T N L C P F G E V F N A T R
GCACACAGCCCCAACATCACCAATCTGTGCCCTTTCGGCGAGGTGTTCAACGCCACCAGA
61 -----!-----!-----!-----!-----!-----! 120

      F A S V Y A W N R K R I S N C V A D Y S
TTCGCTCTGTGTACGCTTGAACCGGAAGCGGATCAGCAATTGCGTGGCCGACTACAGC
121 -----!-----!-----!-----!-----!-----! 180

      V L Y N S A S F S T F K C Y G V S P T K
GTGCTGTACAAACAGCGCCAGCTTCAGCACCTTCAAGTGCACGGCGTGTCCCCIACCAAG
181 -----!-----!-----!-----!-----!-----! 240

      L N D L C F T N V Y A D S F V I R G D E
CTGAACGATCTGTGCTTCACCAACGTGTACGCCGACAGCTTCGTGATCAGAGGCGACGAA
241 -----!-----!-----!-----!-----!-----! 300

      V R Q I A P G Q T G K I A D Y N Y K L P
GTGCGGCAGATTGCCCTGGACAGACAGGCAAGATCGCCGATTACAACATAAGCTGCC
301 -----!-----!-----!-----!-----!-----! 360

      D D F T G C V I A W N S N N L D S K V G
GACGACTTCACCGGCTGTGTGATTGCCTGGAACAGCAACCTGGACAGCAAGTCGGC
361 -----!-----!-----!-----!-----!-----! 420

      G N Y N Y L Y R L F R K S N L K P F E R
GGCAACTACAACCTACCTGTACCGGCTGTTCGGGAAGTCCAACCTGAAGCCTTTCGAGCGG
421 -----!-----!-----!-----!-----!-----! 480

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B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuIgG1 Hinge-CH2-CH3 (SEQ ID NO: 90)

SUBSTITUTE SHEET (RULE 26)

P G S S R G T S P A R M A A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCCTGCCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACC GCCACCAAGGCCTACAACGTGACCAGGCCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCCAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCAGCTAC
901 -----!-----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTCGCCCCAGATCGCCCACTTCGCCCCCAGCCCCAGCCCTTCTTCGGCATGACC
961 -----!-----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACCCGGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGAGCCCCAACTTCAAGGATCAGGTGATCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCCCCACCGAGCCCCAAGAAGGACAAGAGAAGAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGSCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCCGCGC
1201 -----!-----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCAG
1261 -----!-----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCCAATCGTGGCATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGAGCCGAGCGTGTCCTGTTCCCCCCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCCAGGTTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H N A K T K P R E E
TTCAACTGGTACGTGGACGCGCTGGAGGTGCACAACGCCAAGACCAAGGCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCCGCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----!-----! 1680

Figure 11 continued

```

      T I S K A K G Q P R E P Q V Y T L P P S
      ACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCCAGGTGTACACCCTGCCCCCAGC
1681 -----!-----!-----!-----!-----!-----! 1740

      R D E L T K N Q V S L T C L V K G F Y P
      AGAGACAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCCTGGTGAAGGGCTTCTACCCC
1741 -----!-----!-----!-----!-----!-----! 1800

      S D I A V E W E S N G Q P E N N Y K T T
      AGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCAGAGAACAACACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

      P P V L D S D G S F F L Y S K L T V D K
      CCCCCCTGCTGGACAGCGAGCGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

      S R W Q Q G N V F S C S V M H E A L H N
      AGCAGATGGCAGCAGGGCAACGTGTCTCTTGCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
      CACTACACCCAGAAGAGCCTGACCCCTGAGCCCCGCAAGTGATGATCTAAAGCCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040

      PstI
      CGCCCTTAAGGGCTAATCTGCAG
2041 -----!-----!-----!-----!-----!-----! 2064

```

Figure 12: Sequence of pVAXDCSN11; SN11

A: Human IgH Leader + Spike Glycoprotein (AA 330—525) + GS linker + Fibrin v2 Trimer Motif (GTGGGSG)
(SEQ ID NO: 96)

```

      BamHI           M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S P N I T N L C P F G E V F N A T R
      GCACACAGCCCCAACATCACCAATCTGTGCCCTTTCGGCGAGGTGTTCAACGCCACCAGA
61 -----!-----!-----!-----!-----!-----! 120

      F A S V Y A W N R K R I S N C V A D Y S
      TTCGCCCTCTGTGTACGCCCTGGAACCGGAAGCGGATCAGCAATTGCGTGGCCGACTACAGC
121 -----!-----!-----!-----!-----!-----! 180

      V L Y N S A S F S T F K C Y G V S P T K
      GTGCTGTACAACAGCGCCAGCTTCAGCACCTTCAAGTGCTACGGCGTGTCCCCTACCAAG
181 -----!-----!-----!-----!-----!-----! 240

      L N D L C F T N V Y A D S F V I R G D E
      CTGAACGATCTGTGCTTCACCAACGTGTACGCCGACAGCTTCGTGATCAGAGGCGACGAA
241 -----!-----!-----!-----!-----!-----! 300

      V R Q I A P G Q T G K I A D Y N Y K L P
      GTGCGGCAGATTGCCCTGGACAGACAGGCAAGATCCCGATTACAACACTACAACCTGCC
301 -----!-----!-----!-----!-----!-----! 360

      D D F T G C V I A W N S N N L D S K V G
      GACGACTTCACCGGCTGTGTGATTGCCTGGAACAGCAACACCTGGACAGCAAGTTCGGC
361 -----!-----!-----!-----!-----!-----! 420

      G N Y N Y L Y R L F R K S N L K P F E R
      GGCAACTACAACTACCTGTACCGGCTGTTCGGGAAGTCCAACCTGAAGCCTTTCGAGCGG
421 -----!-----!-----!-----!-----!-----! 480

      D I S T E I Y Q A G S T P C N G V E G F
      GACATCAGCACCGAGATCTATCAGGCCCGGACACCCCTTGCAATGGCGTGGGAAGGCTTC
481 -----!-----!-----!-----!-----!-----! 540

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31/121

Figure 12 continued

```

      N C Y F P L Q S Y G F Q P T N G V G Y Q
      AACTGCTACTTCCCACTCCAGTCCCTACGGCTTCCAGCCTACAAACGGCGTGGGCTACCAAG
541 -----!-----!-----!-----!-----!-----! 600

      P Y R V V V L S F E L L H A P A T V C G
      CCTTACAGAGTGGTGGTGGTGGCTTCCAGCTGCTGCATGCTCCTGCTACAGTGTGTGGC
601 -----!-----!-----!-----!-----!-----! 660

      G G S G G G S G G G S G S G Y I P E A P
      GGAGGTTCTGGCGGAGGAAGCGGAGGCGGATCTGGCTCTGGATATATATCCCGAGGCTCCC
661 -----!-----!-----!-----!-----!-----! 720

      R D C Q A Y V R K D G E W V L L S T F L
      AGAGATGCCAGGCCTATGTTCCGAAGGATGGCGAGTGGGTCTGCTGAGCACATTTCTC
721 -----!-----!-----!-----!-----!-----! 780

      G T G G G S G *      XhoI
      GGAACAGCGCGCGGAAGCGGATGATGACTCGAG
781 -----!-----!-----!-----!-----! 813

```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 6)

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      HindIII      M D W I W R I L F L V G A A T G
      AAGCTTGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
      GCACACAGCAGCGACAACGGCCCCCAGAACCCAGAGAAACGGCCCCCAGAAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
      GGCCCCAGCGACGACCGGCAGCAACCCAGAACCGCGAGAGAAAGCGCGCCAGAACCAAG
121 -----!-----!-----!-----!-----!-----! 180

      Q R R P Q G L P N N T A S W F T A L T Q
      CAGAGAAGACCCAGGGCCTGCCCAACAACACCGCCAGCTGGTTACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

      H G K E D L K F P R G Q G V P I N T N S
      CACGGCAAGGAGGACCTGAAGTTCCCGAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

      S P D D Q I G Y Y R R A T R R I R G G D
      AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----! 360

      G K M K D L S P R W Y F Y Y L G T G P E
      GGCAAGATGAAGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

      A G L P Y G A N K D G I I W V A T E G A
      GCGGGCTGCCCTACGGCGCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

      L N T P K D H I G T R N P A N N A A I V
      CTGAACACCCCCAAGGACCACATCGGCACAGAAACCCCGCCAACAACGCCGCCATCTGTG
481 -----!-----!-----!-----!-----!-----! 540

      L Q L P Q G T T L P K G F Y A E G S R G
      CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

      G S Q A S S R S S S R S R N S S R N S T
      GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

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Figure 12 continued

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGACCTCTCCTGCGCGGATGGCTGTTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGAGGGCCAGACTGTGACCAAAAAAGCGCCGCGAGGCCAGCAAGAAGGCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACC GCCAAGGCCTACACGCTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCGAGCAGACCCAGGGCAACTTCGGCGACCAAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTCGCCCCAGATCGCCCACTTCGCCCCAGCCCCAGCCCTTCTTCGCCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAAGACCTTCCCCCCCCACCGAGCCCAAGAAGGACAAGAAGAAGAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAATCGTGCATATAAAGCATACGTGCCCCCTCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTCTGTGTTCCCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGCGTGGAGGTGCACACAGCCTGGACCCAGCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGTGACCCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

Figure 12 continued

```

      T I S K P K G R A Q T P Q V Y T I P P P
1681 ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCCT
-----!-----!-----!-----!-----!-----! 1740

      R E Q M S K K K V S L T C L V T N F F S
1741 AGAGAACAAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCCTGGTGACCAACTTCTTCTCT
-----!-----!-----!-----!-----!-----! 1800

      E A I S V E W E S N G Q P E N N Y K T T
1801 GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCAGAGAACAACACAAAGACCACC
-----!-----!-----!-----!-----!-----! 1860

      P P V L D S D G S F F L Y S K L T V D K
1861 CCCCCCTGCTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
-----!-----!-----!-----!-----!-----! 1920

      S R W Q Q G N V F S C S V M H E A L H N
1921 AGCAGATGGCAGCAGGGCAACGTGTCTCTTGCAGCGTGATGCACGAGGCCCTGCACAAC
-----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
1981 CACTACACCCAGAAGAGCCTGACCCCTGAGCCCCGCAAGTGATGATCTAAAGCCGAATT
-----!-----!-----!-----!-----!-----! 2040

                                PstI
2041 CGCCCTTAAGGGCTAATTCTGCAG
-----!-----!-----!-----!-----! 2064

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Figure 13: Sequence of pVAXDCSN12; SN12

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) + GS linker + Fibrin Trimer Motif (SEQ ID NO: 91)

```

      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I T N L
61 GCACACAGCAGAGTGCAGCCCCACGAGAGCATCGTGAGATPCCCAACATCACCAACCTG
-----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
121 TGCCCCCTCGGCGAGGTGTCAACGCCACAGATTGCGCCAGCGGTACGCCTGGAACAGG
-----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
181 AAGAGMATCAGCAACTGCGTGGCCGACTACAGCGTGTCTACACAGCGCCAGCTTCAGC
-----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F I N V
241 ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTACCAACGTCG
-----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
301 TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAGACC
-----!-----!-----!-----!-----!-----! 360

      G K I A D Y N Y K L P D D F T G C V I A
361 GGCAAGATCGCCGACTACAACCTACAAGCTGCCCCGACGACTTACCGGGCTGCGTGATCGCG
-----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
421 TGGAAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTCTACAGACTG
-----!-----!-----!-----!-----!-----! 480

      F R K S N L K P F E R D I S T E I Y Q A
481 TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCAGATCTACCAGGCC
-----!-----!-----!-----!-----!-----! 540

```

Figure 13 continued

```
      G S T P C N G V E G F N C Y F P L Q S Y
GGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600

      G F Q P T N G V G Y Q P Y R V V V L S F
GGCTTCAGCCCACCAACGGCGTGGGCTACCAAGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660

      E L L H A P A T V C G P K K S T N L V K
GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

      N K C V N F G S G Y I P E A P R D G Q A
AACAAGTGCCTGAACCTTCGGCAGCGGCTACATCCCCGAGGCCCCCAGAGACGGCCAGGCC
721 -----!-----!-----!-----!-----!-----! 780

      Y V R K D G E W V L L S T F L *      XhoI
TACGTGAGAAAGGACGGCGAGTGGGTGCTGCTGTCCACCTCCTGTGATGACTCGAG
781 -----!-----!-----!-----!-----!-----! 837
```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 6)

```
      HindIII      M D W I W R I L F L V G A A T G
AAGCTTGGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCCAGAACCCAGAGAAACGCCCCCAGAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCGAGCAACCAGAACGGCGAGAGAGCGGCGCCAGAAAGCAAG
121 -----!-----!-----!-----!-----!-----! 180

      Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACACCGCCAGCTGGTTCACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

      H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCCCAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

      S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCCAGATCGGCTACTACAGAAGAGCCACCAGAAAGATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----! 360

      G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCGACCGGCCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

      A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCCCCAGGGCGCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

      L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACCCAGAAACCCCGCCAACAACGCCGCCATCGTG
481 -----!-----!-----!-----!-----!-----! 540

      L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600
```

Figure 13 continued

G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCAGCCACCAAGGCTTACAACGTGACCCAGGCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCCAGCAGACCCAGCGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCAGCTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCACCAGGCCAAGAAGGACAAGAAGAAGAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGSGCCCTGCCCCAGAGACAGAAGAAGCAGCAGCAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAATCGTGGGATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCTGTTCCTGTTCCCCCAGGCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACACAGCCTGGACCCAGCCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

Figure 13 continued

```

      N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

      T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCT
1681 -----!-----!-----!-----!-----!-----! 1740

      R E Q M S K K K V S L T C L V T N F F S
AGAGAACAAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

      E A I S V E W E S N G Q P E N N Y K T T
GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

      P P V L D S D G S F F L Y S K L T V D K
CCCCCTGTGCTGGACAGCGACGGCAGCTTCTTCCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

      S R W Q Q G N V F S C S V M H E A L H N
AGCAGATCGCAGCAGCGCAACGTCTTCTCTTGCAGCCTGATCCAGCGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAAT
1981 -----!-----!-----!-----!-----!-----! 2040

      PstI
CGCCCTTAAGGGCTAATCTGCGAG
2041 -----!-----!-----!-----!-----!-----! 2064

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Figure 14: Sequence of pVAXDCSN13; SN13

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) + HuigG1 Hinge-CH2-CH3 (SEQ ID NO: 92)

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      BamHI      M D W I W R I L F L V G A A T G
GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGCTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I T N L
GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCACCTG
61 -----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
TGCCCCCTCGGCGAGGTGTTCAACGCCACCAGATTCCCCAGCGTGACGCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F T N V
ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360

      G K I A D Y N Y K L P D D F T G C V I A
GGCAAGATCGCCGACTACAAGCTGCCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480

```

Figure 14 continued

F R K S N L K P F E R D I S T E I Y Q A
TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540

G S T P C N G V E G F N C Y F P L Q S Y
GGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600

G F Q P T N G V G Y Q P Y R V V V L S F
GGCTTCCAGCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660

E L L H A P A T V C G P K K S T N L V K
GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

N K C V N F E P K S C D K T H T C P P C
AACAAAGTGGCTGAAGTTCGAGCCCAATCGTGCATFAAAACGCATACGTGCCCCCCTGT
721 -----!-----!-----!-----!-----!-----! 780

P A P E L L G G P S V F L F P P K P K D
CCAGCCCAGACTTGCTGGGTGGACCGAGCCTGTTCTGTTCCTCCCAAGCCCAAGGAC
781 -----!-----!-----!-----!-----!-----! 840

T L M I S R T P E V T C V V V D V S H E
ACCCTGATGATCAGCAGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAG
841 -----!-----!-----!-----!-----!-----! 900

D P E V K F N W Y V D G V E V H N A K T
GACCCCGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAACGCCAAGACC
901 -----!-----!-----!-----!-----!-----! 960

K P R E E Q Y N S T Y R V V S V L T V L
AAGCCCAGAGAGGAGCAGTACAACAGCACCTACAGAGTGTGTCCGTGCTGACCGTGTCT
961 -----!-----!-----!-----!-----!-----! 1020

H Q D W L N G K E Y K C K V S N K A L P
CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCC
1021 -----!-----!-----!-----!-----!-----! 1080

A P I E K T I S K A K G Q P R E P Q V Y
GCCCCATCGAGAAGACCATCAGCAAGGCCAAGGGCCAGCCCAGAGAGCCCAGGTGTAC
1081 -----!-----!-----!-----!-----!-----! 1140

T L P P S R D E L T K N Q V S L T C L V
ACCCTGCCCCCAGCAGAGACGAGCTGACCAAGAATCAGGTGAGCCTGACCTGCCTGGTG
1141 -----!-----!-----!-----!-----!-----! 1200

K G F Y P S D I A V E W E S N G Q P E N
AAGGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAACGGCCAGCCCAGAGAAC
1201 -----!-----!-----!-----!-----!-----! 1260

N Y K T T P P V L D S D G S F F L Y S K
AACTACAAGACCACCCCCCGTGTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAG
1261 -----!-----!-----!-----!-----!-----! 1320

L T V D K S R W Q Q G N V F S C S V M H
CTGACCSTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCTCTTGACGCGTGATGCAC
1321 -----!-----!-----!-----!-----!-----! 1380

E A L H N H Y T Q K S L S L S P G K *
GAGGCCCTGCACAACCACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGA
1381 -----!-----!-----!-----!-----!-----! 1440

XhoI
CTCGAG
1441 ----- 1446

Figure 14 continued

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 6)

```

      HindIII      M D W I W R I L F L V G A A T G
AAGCTTGCCACCATGGACTGGATTGGAGAATCCTCTTCCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCCAGAACCCAGAGAAACGCCCCAGAAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCAGCAACCCAGAACGGCGAGAGAACGGCGCCAGAACCAAG
121 -----!-----!-----!-----!-----!-----! 180

      Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACACACCGCCAGCTGGTTCACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

      H G K E D L K F P R G Q G V P I N T N S
CAGGGCAAGGAGGACCTGAAGTTCCCGAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

      S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----! 360

      G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

      A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCGCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

      L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACCCAGAAACCCCGCCAACAACCGCCCATCGTG
481 -----!-----!-----!-----!-----!-----! 540

      L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

      G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

      P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGAACGGCGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

      L A L L L L D R L N Q L E S K M S C K G
CTGGCCCTGCTGCTGGACAGACTGAACCAAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

      Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCCGCAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

      R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

      P E Q T Q G N F G D Q E L I R Q G T D Y
CCCGAGCAGACCCAGGGCAACTTCGGCGACCGAGGAGTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

```

Figure 14 continued

```
      K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTGCCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

      R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

      L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

      A Y K T F P P T E P K K D K K K K A D E
GCCTACAGACCTTCCCCCCCACCGAGCCCAAGAAGGACAAGAAGAAGAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

      T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

      D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCAG
1261 -----!-----!-----!-----!-----!-----! 1320

      A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAATCGTGCATATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

      L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTCTGTTCCTGTTCCCCCAAGCCCAAGGACACCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

      R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

      F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACACAGCCTGGACCCAGCCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

      Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

      N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

      T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCT
1681 -----!-----!-----!-----!-----!-----! 1740

      R E Q M S K K K V S L T C L V T N F F S
AGAGAACAAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

      E A I S V E W E S N G Q P E N N Y K T T
GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAATAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

      P P V L D S D G S F F L Y S K L T V D K
CCCCCGTGTGGACAGCGAGGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920
```

40/121

Figure 14 continued

```
      S R W Q Q G N V F S C S V M H E A L H N
AGCAGATGGCAGCAGGGCAACGTGTTCTCTTGACGCTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040

              PstI
CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----!-----! 2064
```

Figure 15: Sequence of pVAXDCSN14; SN14

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 97)

```
      BamHI           M D W I W R I L F L V G A A T G
GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I T N L
GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAACCTG
61 -----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
TGCCCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCCAGCGTGACGCCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F T N V
ACTTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
TACGCCGACAGCTTCGTGATCAGAGCGACGAGGTGAGACAGATCGCCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360

      G K I A D Y N Y K L P D D F T G C V I A
GGCAAGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480

      F R K S N L K P F E R D I S T E I Y Q A
TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540

      G S T P C N G V E G F N C Y F P L Q S Y
GGCAGCACCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600

      G F Q P T N G V C Y Q P Y R V V V L S F
GGCTTCCAGCCCACCAACGGCGTGGGCTACCAAGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660

      E L L H A P A T V C G P K K S T N L V K
GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720
```

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Figure 15 continued

```
      N K C V N F E P K S C D K T H T C P P C
721  AACAAGTGCCTGAACTTCGAGCCCAAGAGCTGTGACAAAACACATACATGCCCCCCTGC
-----!-----!-----!-----!-----!-----! 780

      P A P E L L G G P S V F L F P P K P K D
781  CCTGCCCTGAGTGCTTGGGGGCCCATCTGTGTTCTGTCCCCCAAGCCAAGGAC
-----!-----!-----!-----!-----!-----! 840

      T L M I S R T P E V T C V V V D V S H E
841  ACCCTGATGATCAGCAGAACCCTGAGGTGACCTGTGTGGTGGTGGATGTGAGCCATGAG
-----!-----!-----!-----!-----!-----! 900

      D P E V K F N W Y V D G V E V H T A W T
901  GACCCTGAGGTGAAGTTCAACTGGTATGTGGATGGGTGGAGGTGCACACAGCCTGGACA
-----!-----!-----!-----!-----!-----! 960

      Q P R E E Q Y N S T Y R V V S V L I V L
961  CAGCCTAGAGAGGAGCAGTACAACAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGCTG
-----!-----!-----!-----!-----!-----! 1020

      H Q D W L N G K E Y K C K V S N K A L P
1021  CACCAAGACTGCCTGAATGGCAAGGACTACAAGTCCAAGGTGACCAACAAGGCCCTGCCT
-----!-----!-----!-----!-----!-----! 1080

      A P I E K T I S K P K G R A Q T P Q V Y
1081  GCCCCATTGAGAAGACCATCAGCAAGCCCAAGGGCAGAGTCAGACCCCCAAGTGATAC
-----!-----!-----!-----!-----!-----! 1140

      T I P P P R E Q M S K K K V S L T C L V
1141  ACCATCCCCCCTAGAGAGCAGATGAGCAAGAAGGTGAGCCTGACCTGCCTGGTG
-----!-----!-----!-----!-----!-----! 1200

      T N F F S E A I S V E W E S N G Q P E N
1201  ACCAACITCTCTCTGAGGCCATCTCTGTGGAGTGGGAGAGCAATGGGCAGCCTGAGAAC
-----!-----!-----!-----!-----!-----! 1260

      N Y K T T P P V L D S D G S F F L Y S K
1261  AACTACAAGACCACCCCCCTGTGCTGGACTCTGATGGCAGCTTCTTCTGTACAGCAAG
-----!-----!-----!-----!-----!-----! 1320

      L T V D K S R W Q Q G N V F S C S V M H
1321  CTGACAGTGGACAAGAGCAGATGGCAGCAAGGCAATGTGTTACAGCTGCTCTGTGATGCAT
-----!-----!-----!-----!-----!-----! 1380

      E A L H N H Y T Q K S L S L S P G K *
1381  GAGGCCCTGCACAACCACTACACACAGAAGAGCCTGAGCCTGAGCCCTGGCAAGTGATGA
-----!-----!-----!-----!-----!-----! 1440

      XhoI
      CTCGAG
1441 ----- 1446
```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 6)

```
      HindIII      M D W I W R I L F L V G A A T G
      AAGCTTGGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

      A H S S D N G P Q N Q R N A P R I T F G
61  GCACACAGCAGCGACAACGGCCCCCAGAACCAAGAGAAACGGCCCCAGAAATCACCTTCGGC
-----!-----!-----!-----!-----!-----! 120

      G P S D S T G S N Q N G E R S G A R S K
121  GGCCCCAGCGACAGCACCGGCAACCAAGCAACGGCCAGAGAAAGCGCGCCAGAAAGCAAG
-----!-----!-----!-----!-----!-----! 180
```

Figure 15 continued

Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACACGCCAGCTGGTTACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCCCAGAGGCCAGGGCTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGGCAG
301 -----!-----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
GCCGGCCTGCCCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCAAGCACCATCGGCACCAGAAACCCGCCAACAACCGGCCCATCGTG
481 -----!-----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGTGGCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

G S Q A S S R S S S R S R N S S R N S T
GGAGCCAGGCCTCAAGCCGTTCCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCTTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCAGCAGACCCAGGGCAACTTCGGCGACCAAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTCGCCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCAAGCGGACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D E K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCACCAGGCCAAGAAGGACAAGAAGAAGAGGCGGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

Figure 15 continued

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCGCCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAAATCGTGCGATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G C P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCCTGTCCCCCAAGCCCAAGGACACCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H T A W T Q P R E E
TTCAACTCGTACCTGCACGGCGTGGAGGTGCACACACCTGCACCCAGCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCT
1681 -----!-----!-----!-----!-----!-----! 1740

R E Q M S K K K V S L T C L V T N F F S
AGAGAACAAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

E A I S V E W E S N G Q P E N N Y K T T
GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

P P V L D S D G S F F L Y S K L T V D K
CCCCCGTGTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

S R W Q Q G N V F S C S V M H E A L H N
AGCAGATGGCAGCAGGGCAACGTGTTCTCTTGACCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

H Y T Q K S L S L S P G K *
CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040

PstI
CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----! 2064

Figure 16:

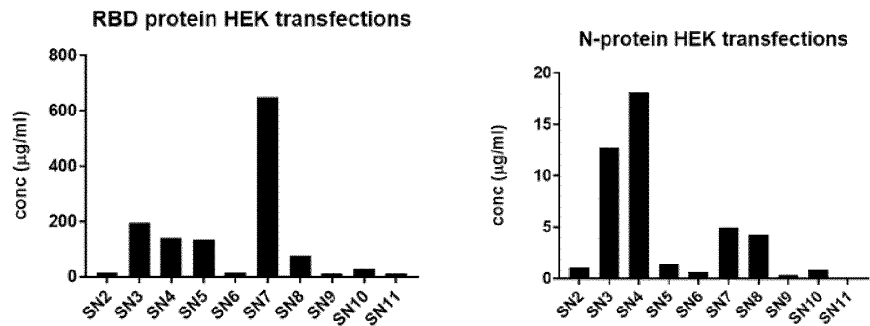


Figure 17

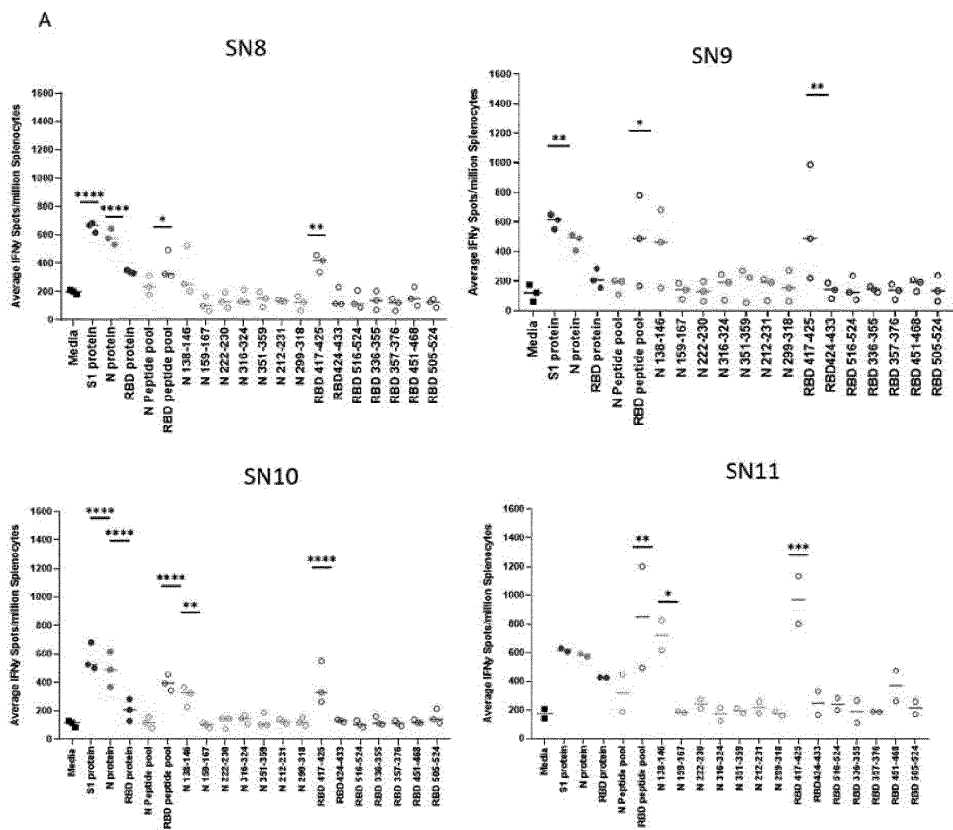


Figure 17

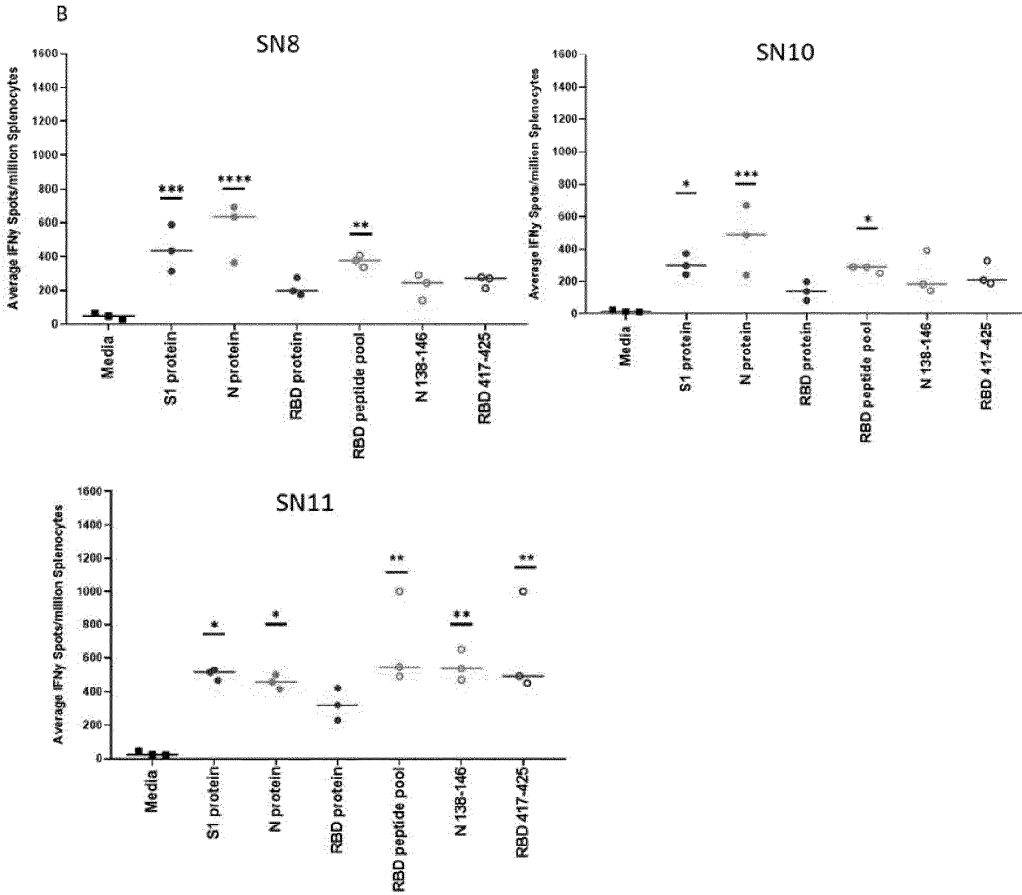


Figure 18

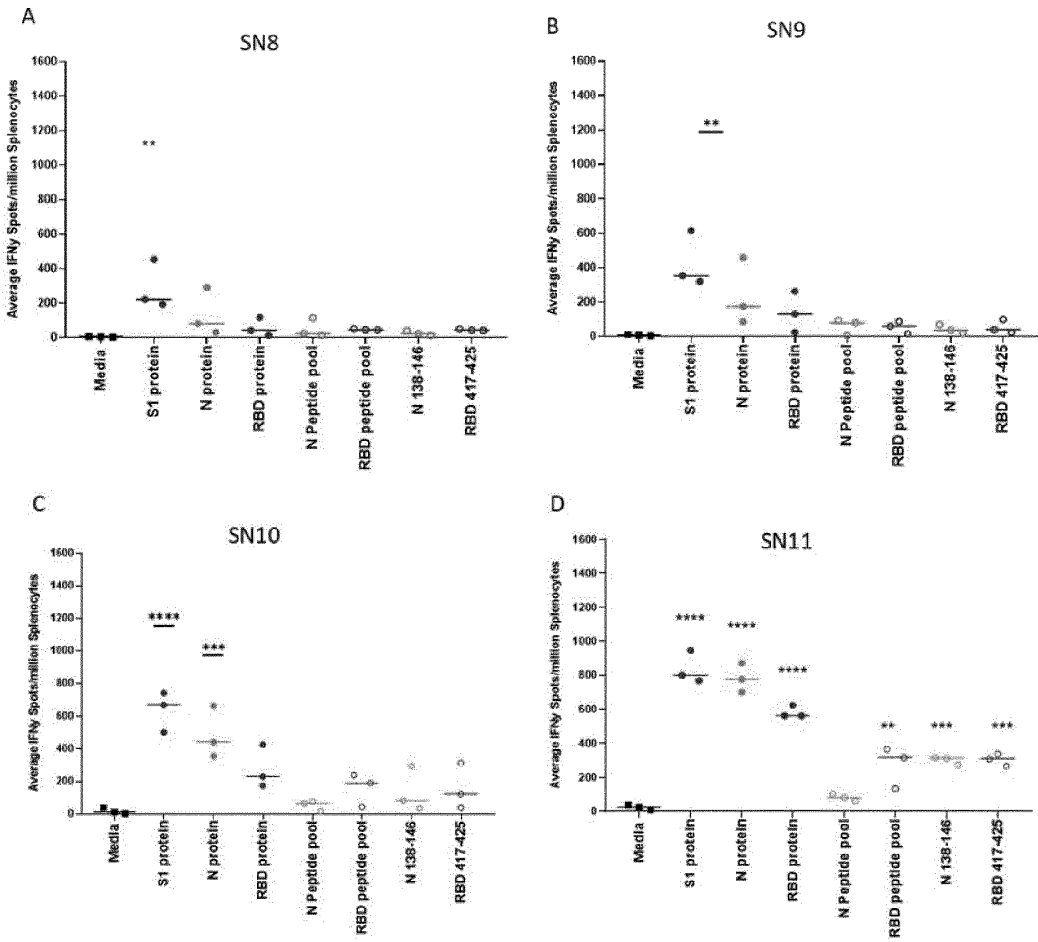


Figure 19

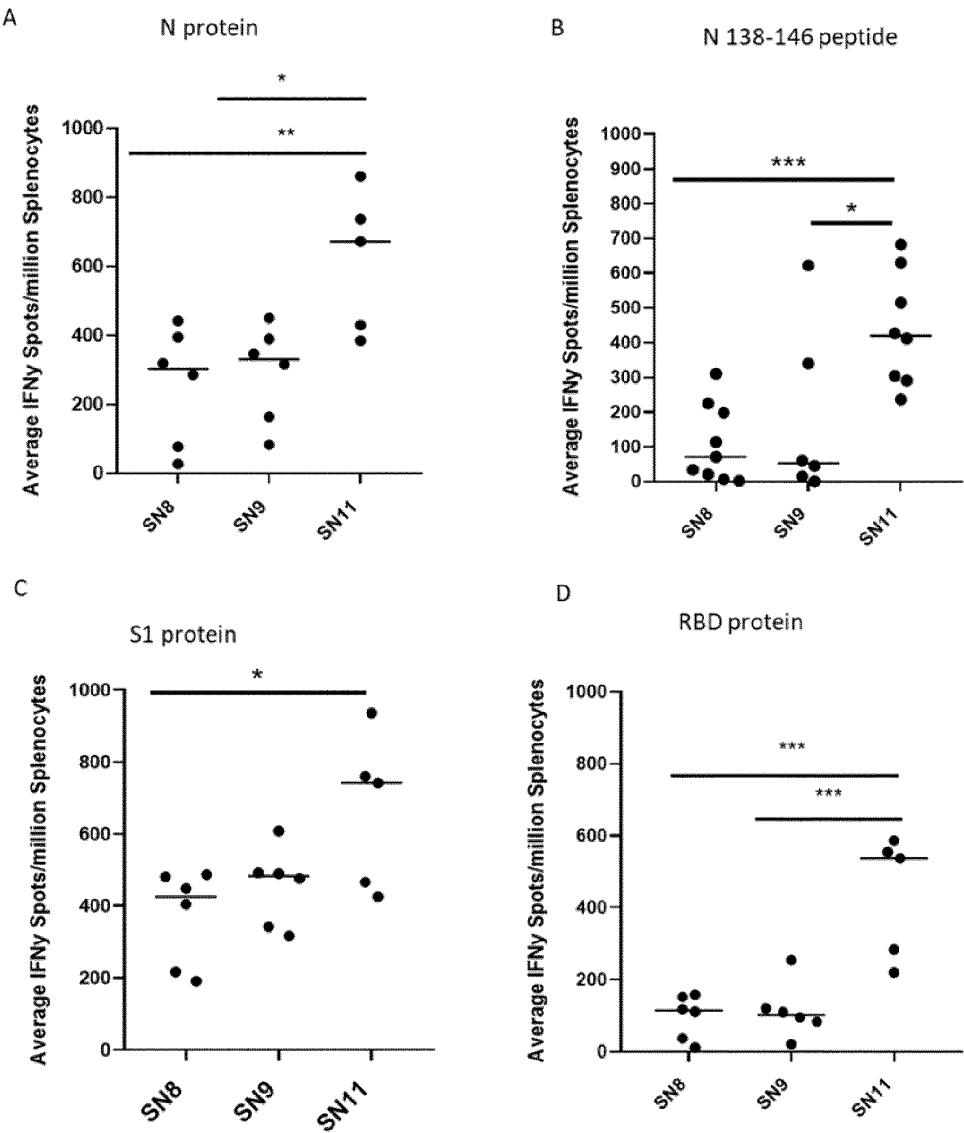


Figure 20

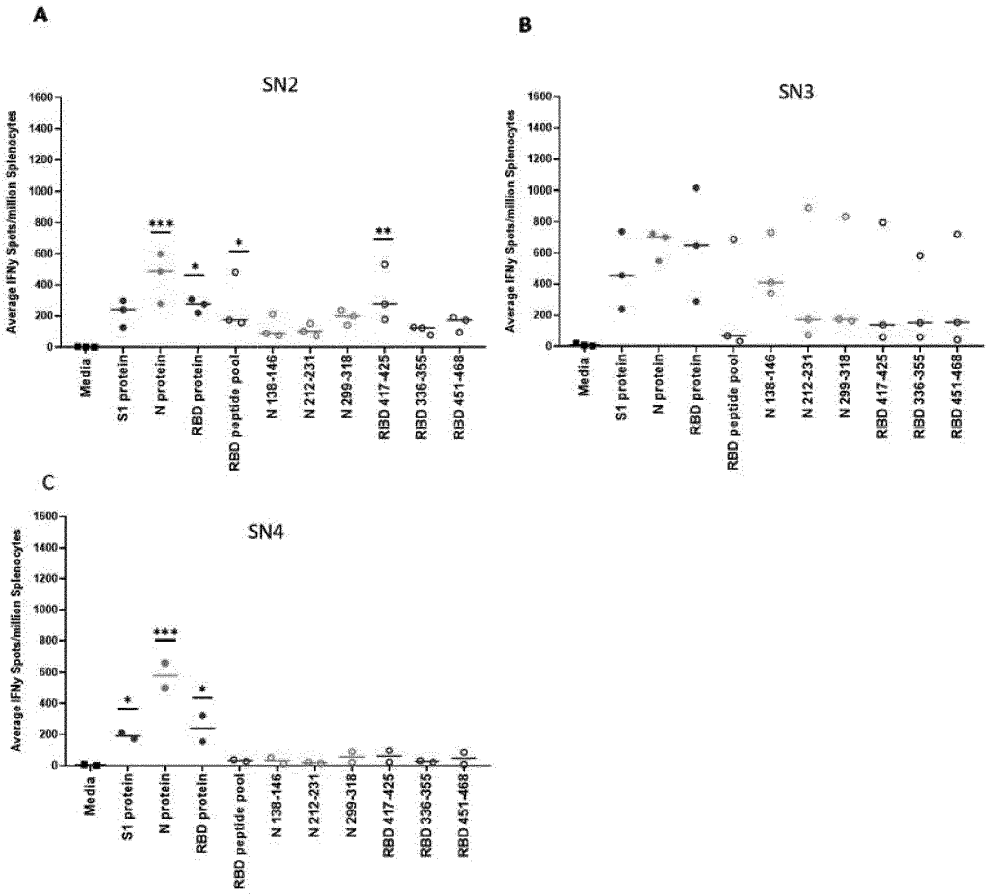


Figure 21

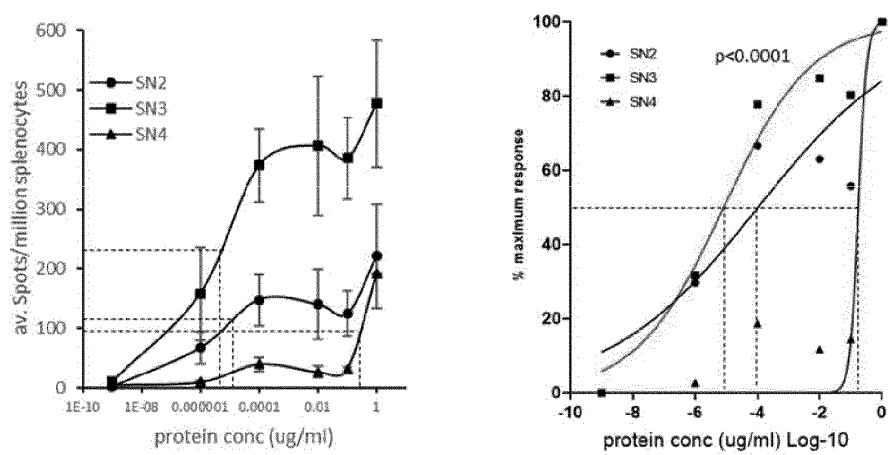


Figure 22

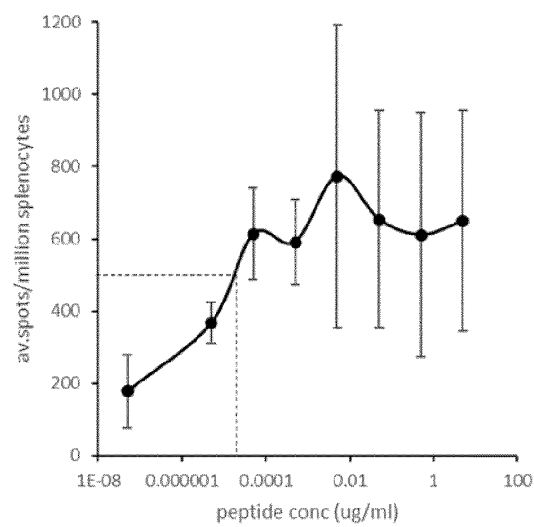


Figure 23

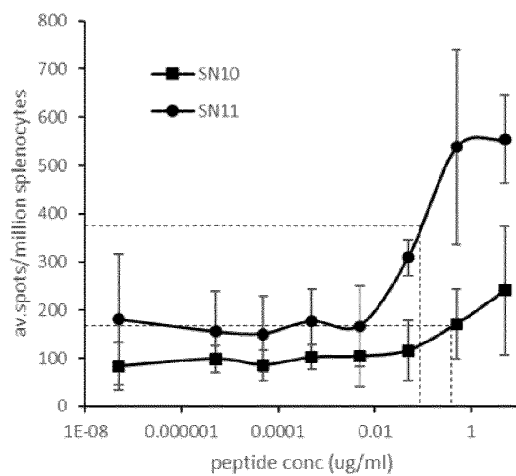


Figure 24

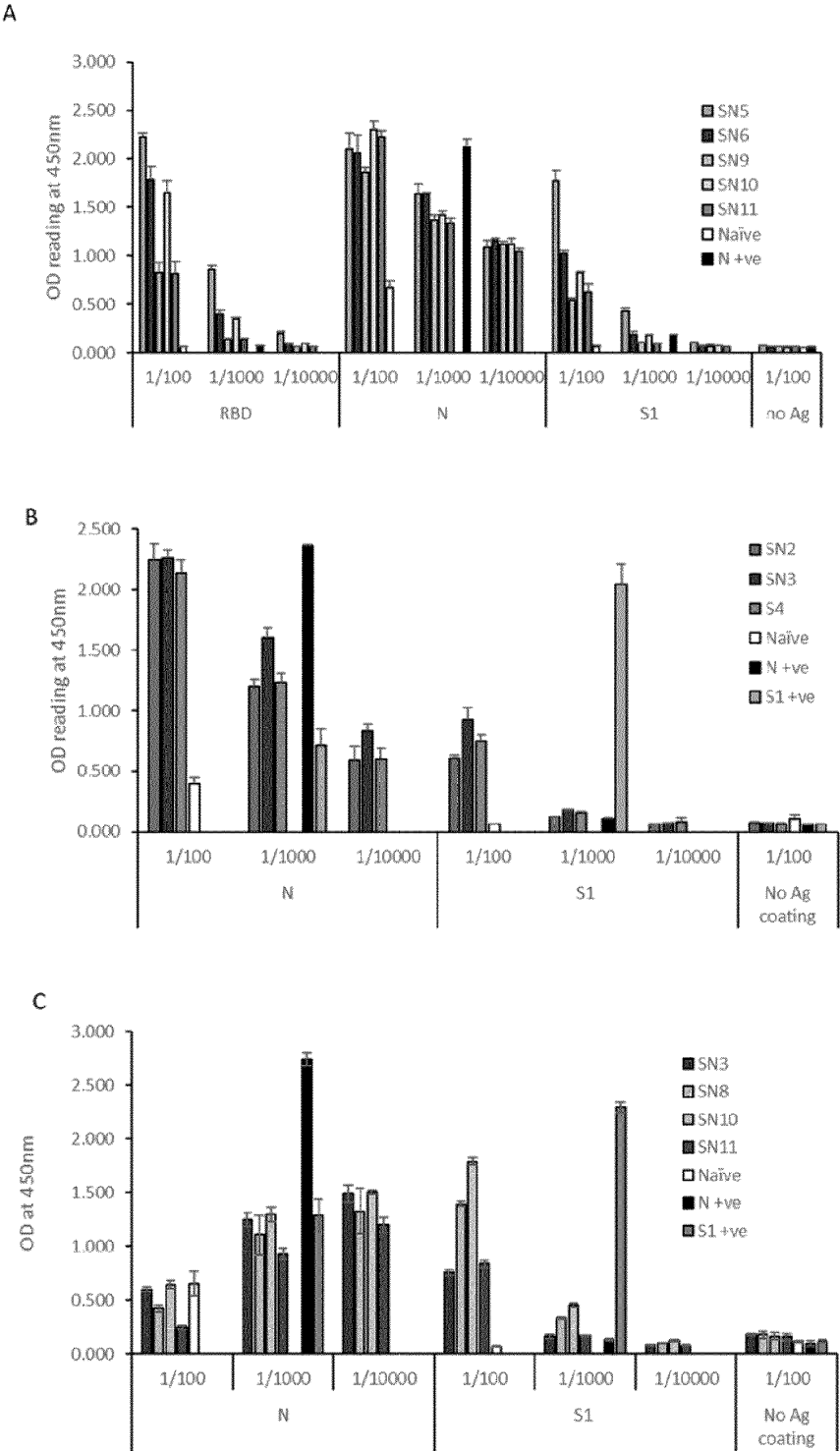


Figure 25

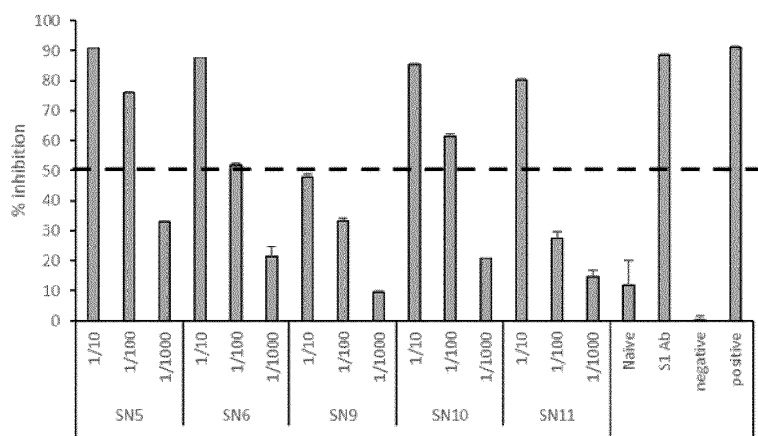


Figure 26

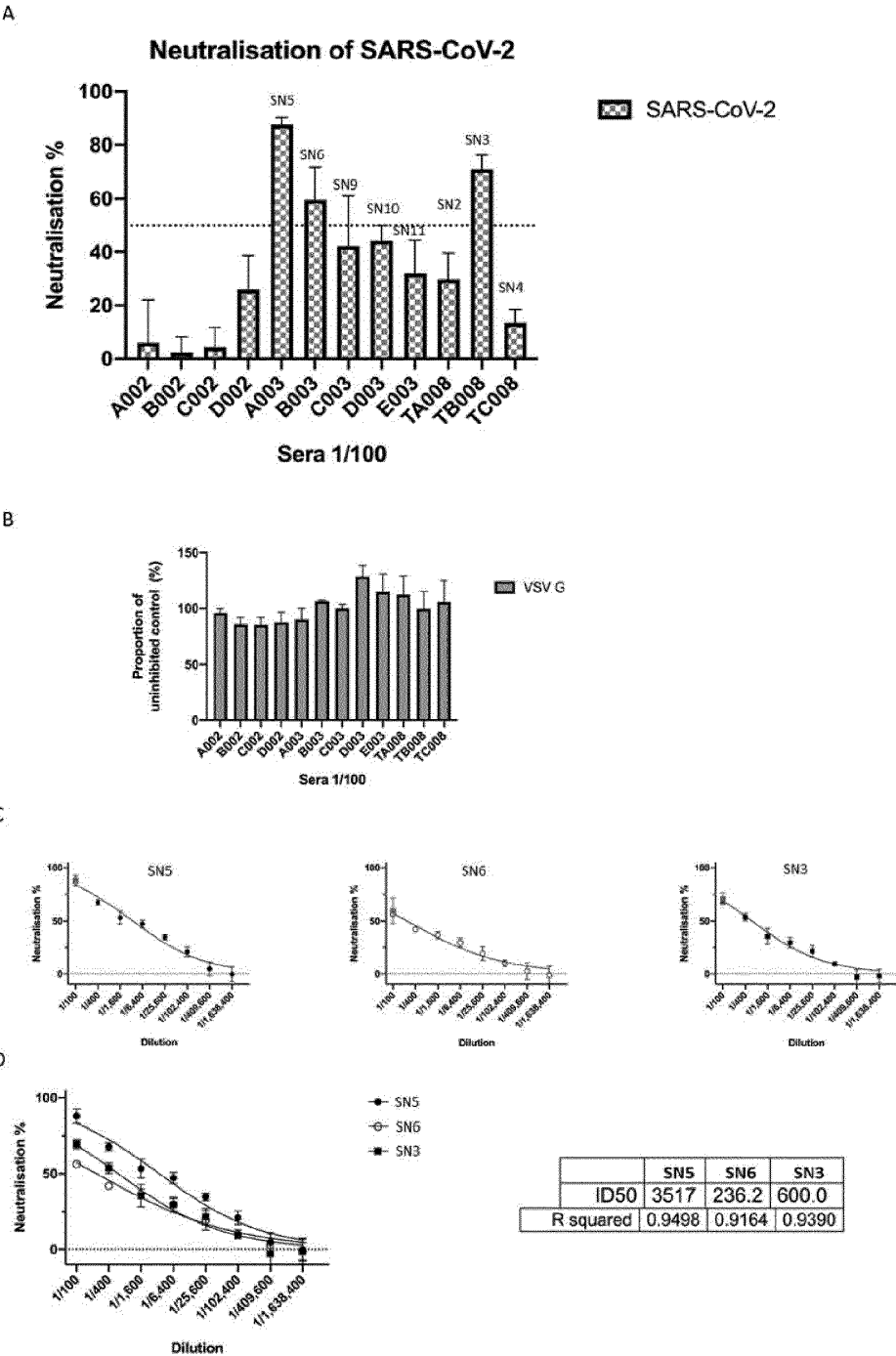


Figure 27: Sequence of pVAXDCSN15; SN15

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) (SEQ ID NO: 89)

```
BamHI      M D W I W R I L F L V G A A T G
GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60

  A H S R V Q P T E S I V R F P N I T N L
  GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAACCTG
61  -----!-----!-----!-----!-----!-----! 120

  C P F G E V F N A T R F A S V Y A W N R
  TGCCCCCTCGGCGAGGTGTCAACGCCACCAGATTGCGCCAGCGTGTACGCCTGGAACAGG
121  -----!-----!-----!-----!-----!-----! 180

  K R I S N C V A D Y S V L Y N S A S F S
  AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181  -----!-----!-----!-----!-----!-----! 240

  T F K C Y G V S P T K L N D L C F T N V
  ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241  -----!-----!-----!-----!-----!-----! 300

  Y A D S F V I R G D E V R Q I A P G Q T
  TAGCCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCCGGCCAGACC
301  -----!-----!-----!-----!-----!-----! 360

  G K I A D Y N Y K L P D D F T G C V I A
  GGCAAGATCGCCGACTACAACACAAGCTGCCCGACGACTTCACCGGCTGCGTGATCGCG
361  -----!-----!-----!-----!-----!-----! 420

  W N S N N L D S K V G G N Y N Y L Y R L
  TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACACCTCTACAGACTG
421  -----!-----!-----!-----!-----!-----! 480

  F R K S N L K P F E R D I S T E I Y Q A
  TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481  -----!-----!-----!-----!-----!-----! 540

  G S T P C N G V E G F N C Y F P L Q S Y
  GGCAGCACCCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541  -----!-----!-----!-----!-----!-----! 600

  G F Q P T N G V G Y Q P Y R V V V L S F
  GGCTTCCAGCCCACCAACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGCTTC
601  -----!-----!-----!-----!-----!-----! 660

  E L L H A P A T V C G P K K S T N L V K
  GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGCACCAATCTGGTGAAG
661  -----!-----!-----!-----!-----!-----! 720

  N K C V N F * XhoI
  AACAAGTGCCTGAACCTCTGATGACTCGAG
721  -----!-----!-----! 750
```

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 6)

```
HindIII      M D W I W R I L F L V G A A T G
AAGCTTGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1  -----!-----!-----!-----!-----!-----! 60
```

Figure 27 continued

A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCCAGAACCCAGAGAAACGCCCCCAGAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACGACCGGGCAGCAACCAGAACGGCGAGAGAAGCGGGCCAGAACGAAG
121 -----!-----!-----!-----!-----!-----! 180

Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACCCGCCAGCTGGTTACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCCCAGAGGGCAGGGCGTGGCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGGCCACCAGAAGAATCAGAGGCGGGCAGC
301 -----!-----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
GGCGGCCTGCCCTACGGCGCCAAACAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACCAGAAACCCGCCAACACGCGCCATCGTG
481 -----!-----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCGAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCGCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L L L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCAGCCACCAAGGCCTACAACGTGACCCAGGCCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCGAGCAGACCCAGGGCAACTTCGGCGACCCAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

Figure 27 continued

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTGCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCGAGCGGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCCCCAGCGCCCAAGAGGACAAGAAGAAGAAGGCCGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCGCGCGC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E P K S C D K T H T C P P C P A P E L
GCCGAGCCCAATCGTGCGATAAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCCTGTTCCCCCAGCCCAAGGACACCCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACACAGCCTGGACCCAGCCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCCCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCT
1681 -----!-----!-----!-----!-----!-----! 1740

R E Q M S K K K V S L T C L V T N F F S
AGAGAACAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

E A I S V E W E S N G Q P E N N Y K T T
GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCCGAGAACAACACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

Figure 27 continued

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      P P V L D S D G S F F L Y S K L T V D K
      CCCCCGTGGACAGCGACGGCAGCTTCTTCTTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920
      S R W Q Q G N V F S C S V M H E A L H N
      AGCAGATGGCAGCAGGGCAACGTGTTCTTGCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980
      H Y T Q K S L S L S P G K *
      CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040
              PstI
      CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----!-----! 2064

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Figure 28: Sequence of pVAXDCIB68 (SCIB1)

A: Heavy Variable + HuigG1 CH1-Hinge-CH2-CH3 (SEQ ID NO: 98)

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HindIII M G W S C I I L F L V A T A T G V
AAGCTT ACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
 1 -----!-----!-----!-----!-----!-----! 60
      H S Q V Q L V E T G G G L I Q P G G S L
      CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTG
61 -----!-----!-----!-----!-----!-----! 120
      R M S C G T G R A M L G T H T M E V T V
      AGAATGTCCTGTGGGACAGGCAGGGCAATGCTGGGCACACACACCATGGAAGTAACTGTC
121 -----!-----!-----!-----!-----!-----! 180
      Y H W V R Q A P G K G L E W I A Y I G S
      TACCATGGGTTCCGCCAGGCTCCGGGAAGGGGCTGGAGTGGATCGCATACATTGGTAGT
181 -----!-----!-----!-----!-----!-----! 240
      G G S V Y D F F V W L R F T I S R D N S
      GGTGGTAGTGTATGATTTTTTGTGTGGCTCCGATTACCATTTCCAGAGACAATAGC
241 -----!-----!-----!-----!-----!-----! 300
      K N T L Y L Q L N S L R A E D T A V Y Y
      AAGAACACCCTGTATTTGCAATTGAACAGTCTGAGGGCTGAGGACACAGCCGTGTATTAC
301 -----!-----!-----!-----!-----!-----! 360
      C A R W N R Q L Y P E W T E A Q R L D W
      TCGCCCCGATGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCAGAGACTTGACTGG
361 -----!-----!-----!-----!-----!-----! 420
              AfeI
      G Q G T T V T V S S A S T K G P S V F P
      GGCCAAGGAACCACGGTCACCGTCTCCAGCGCTTCCACCAAGGGCCCATCGGTCTTCCCC
421 -----!-----!-----!-----!-----!-----! 480

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Figure 28 continued

L A P S S K S T S G G T A A L G C L V K
CTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG
481 -----!-----!-----!-----!-----!-----! 540

D Y F P E P V T V S W N S G A L T S G V
GACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTG
541 -----!-----!-----!-----!-----!-----! 600

H T F P A V L Q S S G L Y S L S S V V T
CACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
601 -----!-----!-----!-----!-----!-----! 660

V P S S S L G T Q T Y I C N V N H K P S
GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGC
661 -----!-----!-----!-----!-----!-----! 720

N T K V D K K V E P K S C D K T H T C P
AACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTAACAACTCACACATGCCCA
721 -----!-----!-----!-----!-----!-----! 780

P C P A P E L L G G P S V F L F P P K P
CCGTGCCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCC
781 -----!-----!-----!-----!-----!-----! 840

K D T L M I S R T P E V T C V V V D V S
AAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGC
841 -----!-----!-----!-----!-----!-----! 900

H E D P E V K F N W Y V D G V E V H N A
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
901 -----!-----!-----!-----!-----!-----! 960

K T K P R E E Q Y N S T Y R V V S V L T
AAGACAAAGCCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACC
961 -----!-----!-----!-----!-----!-----! 1020

V L H Q D W L N G K E Y K C K V S N K A
GTCTTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAGCC
1021 -----!-----!-----!-----!-----!-----! 1080

L P A P I E K T I S K A K G Q P R E P Q
CTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
1081 -----!-----!-----!-----!-----!-----! 1140

V Y T L P P S R D E L T K N Q V S L T C
GTGTACACCCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGC
1141 -----!-----!-----!-----!-----!-----! 1200

L V K G F Y P S D I A V E W E S N G Q P
CTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG
1201 -----!-----!-----!-----!-----!-----! 1260

E N N Y K T T P P V L D S D G S F F L Y
GAGAACAACCTACAAGACCAGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTAC
1261 -----!-----!-----!-----!-----!-----! 1320

S K L T V D K S R W Q Q G N V F S C S V
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
1321 -----!-----!-----!-----!-----!-----! 1380

Figure 28 continued

M H E A L H N H Y T Q K S L S L S P G K
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
1381 -----!-----!-----!-----!-----!-----! 1440

* **EcoRI**
TGATCTAAAGGGCGAATTTCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----!-----! 1477

B: Light Variable + Human kappa constant (SEQ ID NO: 99)

BamHI M G W S C I I L F L V A T A T G V
GGATCCACCATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

H S D V L M T Q S P L S L P V T P G E P
CACTCCGATGTGTGATGACCCAACTCTCCACTCTCCCTGCCTGTCACTCCTGGGGAGCCA
61 -----!-----!-----!-----!-----!-----! 120

A S I S C W N R Q L Y P E W T E A Q R L
GCCTCGATCTCTTGGTGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCCAGAGACTT
121 -----!-----!-----!-----!-----!-----! 180

D W Y L Q K P G Q S P Q L L I Y K V S N
GACTGGTATCTGCAGAAACAGGCCAGTCTCCACAGCTCCTGATCTACAAAGTTTCCAAC
181 -----!-----!-----!-----!-----!-----! 240

R F S G V P D R F S G S G S G T D F T L
CGATTTTCTGGGGTCCCAGACAGATTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTC
241 -----!-----!-----!-----!-----!-----! 300

K I S R V E A E D T G V Y Y C G T G R A
AAGATCAGCAGAGTGGAGGCTGAGGATACCGGAGTGTATTACTGCGGACAGGCAGGGCA
301 -----!-----!-----!-----!-----!-----! 360

M L G T H T M E V T V Y H F G G G T K V
ATGCTGGGCACACACCATGGAAGTGACTGTCTACCATTTTCGGTGGAGGCACCAAGGTG
361 -----!-----!-----!-----!-----!-----! 420

BsiWI
E I K R T V A A P S V F I F P P S D E Q
GAAATCAAGCGTACGGTAGCGGCCCATCTGTCTTCATCTTCCGCCATCTGATGAGCAG
421 -----!-----!-----!-----!-----!-----! 480

L K S G T A S V V C L L N N F Y P R E A
TTGAAATCTGGAAGTGCCTCTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC
481 -----!-----!-----!-----!-----!-----! 540

K V Q W K V D N A L Q S G N S Q E S V T
AAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCA
541 -----!-----!-----!-----!-----!-----! 600

E Q D S K D S T Y S L S S T L T L S K A
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA
601 -----!-----!-----!-----!-----!-----! 660

Figure 28 continued

```

      D Y E K H K V Y A C E V T H Q G L S S P
      GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCC
661 -----!-----!-----!-----!-----!-----! 720

      V T K S F N R G E C * XhoI
      GTCACAAAGAGCTTCAACAGGGGAGAGTGTGACTCGAG
721 -----!-----!-----!-----!-----!-----! 759

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Figure 29: Sequence of pVAXDCIB68 iV1 (iCIB1)

A: Heavy Variable + HuigG1 CH1-Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold)

(SEQ ID NO: 100)

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HindIII M G W S C I I L F L V A T A T G V
      AAGCTTACCATTGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

      H S Q V Q L V E T G G G L I Q P G G S L
      CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTG
61 -----!-----!-----!-----!-----!-----! 120

      R M S C G T G R A M L G T H T M E V T V
      AGAATGTCCTGTGGGACAGGCAGGGCAATGCTGGGCACACACCATGGAAGTAACTGTC
121 -----!-----!-----!-----!-----!-----! 180

      Y H W V R Q A P G K G L E W I A Y I G S
      TACCAITGGGTTCCGCCAGGCTCCGGGAAGGGGCTGGAGTGGATCGCATACATTGGTAGT
181 -----!-----!-----!-----!-----!-----! 240

      G G S V Y D F F V W L R F T I S R D N S
      GGTGGTAGTGTATGATTTTGTGTGGCTCCGATTCAACATTTCCAGAGACAATAGC
241 -----!-----!-----!-----!-----!-----! 300

      K N T L Y L Q L N S L R A E D T A V Y Y
      AAGAACACCTGTATTTGCAATTGAACAGTCTGAGGGCTGAGGACACAGCCGTGTATTAC
301 -----!-----!-----!-----!-----!-----! 360

      C A R W N R Q L Y P E W T E A Q R L D W
      TGCGCCCGATGGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCCAGAGACTTGACTGG
361 -----!-----!-----!-----!-----!-----! 420

      AfeI
      G Q G T T V T V S S A S T K G P S V F P
      GGCCAAGGAACACGGTCACCGTCTCCAGCGCTTCCACCAAGGGCCCATCGGTCTTCCCC
421 -----!-----!-----!-----!-----!-----! 480

      L A P S S K S T S G G T A A L G C L V K
      CTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG
481 -----!-----!-----!-----!-----!-----! 540

      D Y F P E P V T V S W N S G A L T S G V
      GACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGCGTG
541 -----!-----!-----!-----!-----!-----! 600

      H T F P A V L Q S S G L Y S L S S V V T
      CACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC

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61/121

601 -----!-----!-----!-----!-----!-----! 660
Figure 29 continued

V P S S S L G T Q T Y I C N V N H K P S
GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGC
661 -----!-----!-----!-----!-----!-----! 720
N T K V D K K V E P K S C D K T H T C P
AACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA
721 -----!-----!-----!-----!-----!-----! 780
P C P A P E L L G G P S V F L F P P K P
CCGTGCCAGCACCTGAACCTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCC
781 -----!-----!-----!-----!-----!-----! 840
K D T L M I S R T P E V T C V V V D V S
AAGGACACCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGC
841 -----!-----!-----!-----!-----!-----! 900
H E D P E V K F N W Y V D G V E V H T A
CAGGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATACAGCC
901 -----!-----!-----!-----!-----!-----! 960
W T Q P R E E Q Y N S T Y R V V S V L T
TGGACACAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCACC
961 -----!-----!-----!-----!-----!-----! 1020
V L H Q D W L N G K E Y K C K V S N K A
GTCTTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAGGCC
1021 -----!-----!-----!-----!-----!-----! 1080
L P A P I E K T I S K P K G R A Q T P Q
CTCCAGCCCCCATCGAGAAAACCATCTCCAACCCAAAGGGAGAGCCCAGACACCACAG
1081 -----!-----!-----!-----!-----!-----! 1140
V Y T I P P P R E Q M S K K K V S L T C
GTGTACACCATACCCCACCTCGGGAACAAATGTCCAAGAAGAAGGTGAGCCTGACCTGC
1141 -----!-----!-----!-----!-----!-----! 1200
L V T N F F S E A I S V E W E S N G Q P
CTGGTCACCAACTTCTTCTCTGAAGCCATCAGTGTGGAGTGGGAGAGCAATGGGCAGCCG
1201 -----!-----!-----!-----!-----!-----! 1260
E N N Y K T T P P V L D S D G S F F L Y
GAGAACAACCTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTAC
1261 -----!-----!-----!-----!-----!-----! 1320
S K L T V D K S R W Q Q G N V F S C S V
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
1321 -----!-----!-----!-----!-----!-----! 1380
M H E A L H N H Y T Q K S L S L S P G K
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
1381 -----!-----!-----!-----!-----!-----! 1440
* EcoRI
TGATCTAAAGGGCGATATCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----! 1477

SUBSTITUTE SHEET (RULE 26)

Figure 29 continued

B: Light Variable + Human kappa constant (SEQ ID NO: 99)

BamHI M G W S C I I L F L V A T A T G V
GGATCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----! 60

H S D V L M T Q S P L S L P V T P G E P
CACTCCGATGTGTGATGACCCAATCTCCACTCTCCCTGCCTGTCACTCCTGGGGAGCCA
61 -----!-----!-----!-----!-----! 120

A S I S C W N R O L Y P E W T E A O R L
GCCTCGATCTCTTGCTGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCCAGAGACTT
121 -----!-----!-----!-----!-----! 180

D W Y L Q K P G Q S P Q L L I Y K V S N
GACTGGTATCTGCAGAAACCAGGCCAGTCTCCACAGCTCCTGATCTACAAAGTTTCCAAC
181 -----!-----!-----!-----!-----! 240

R F S G V P D R F S G S G S G T D F T L
CGATTTTCTGGGGTCCCAGACAGATTCACTGGCAGTGGATCAGGGACAGATTTCACACTC
241 -----!-----!-----!-----!-----! 300

K I S R V E A E D T G V Y Y C G T G R A
AAGATCAGCAGAGTGGAGGCTGAGGATACCGGAGTGTATTACTGCGGACAGGCAGGGCA
301 -----!-----!-----!-----!-----! 360

M L G T H T M E V T V Y H F G G G T K V
ATGCTGGGCACACACACCATGGAAGTGACTGTCTACCATTTTCGGTGGAGGCACCAAGGTG
361 -----!-----!-----!-----!-----! 420

BsiWI
E I K R T V A A P S V F I F P P S D E Q
GAAATCAAGCGTACGGTAGCGGCCCCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAG
421 -----!-----!-----!-----!-----! 480

L K S G T A S V V C L L N N F Y P R E A
TTGAAATCTGGAAGTGCCTCTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC
481 -----!-----!-----!-----!-----! 540

K V Q W K V D N A L Q S G N S Q E S V T
AAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACACA
541 -----!-----!-----!-----!-----! 600

E Q D S K D S T Y S L S S T L T L S K A
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA
601 -----!-----!-----!-----!-----! 660

D Y E K H K V Y A C E V T H Q G L S S P
GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCC
661 -----!-----!-----!-----!-----! 720

V T K S F N R G E C * **XhoI**
GTCAAAAGAGCTTCAACAGGGGAGAGTGTGACTCGAG
721 -----!-----!-----!-----!-----! 759

Figure 30: Sequence of pVAXDCIB238 (SCIB1plus)

A: Heavy Variable + HuIgG1 CH1-Hinge-CH2-CH3 (SEQ ID NO: 101)

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HindIII  M G W S C I I L F L V A T A T G V
AAGCTT ACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1  -----!-----!-----!-----!-----!-----! 60

      H S Q V Q L V E T G G G L I Q P G G S L
      CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAA'CCAGCCTGGAGGGTCCCTG
61  -----!-----!-----!-----!-----!-----! 120

      R M S C   G T G R A M L G T H T M E V T V
      AGAATGTCTCTGGGACAGGCAGGGCAATGCTGGGCACACACCATGGAAGTGACTGTC
121 -----!-----!-----!-----!-----!-----! 180

      Y H   W V R Q A P G K G L E W I A Y I G S
      TACCATGGGTTCCGGCAGGCTCCGGGAAGGGGCTGGAGTGGATCGCATACATTGGTAGT
181 -----!-----!-----!-----!-----!-----! 240

      G G   S V Y D F F V W L   R F T I S R D N S
      GGTGGTAGTGTATGATTTTTTTGTGTGGCTCCGATTACCATTTCCAGAGACAATAGC
241 -----!-----!-----!-----!-----!-----! 300

      K N T I Y L Q L N S L R A E D T A V Y Y
      AAGAACACCCTGTATTTGCAATTGAACAGTCTGAGGGCTGAGGACACAGCCGTGTATTAC
301 -----!-----!-----!-----!-----!-----! 360

      C A R   V P L D C V L Y R Y G S F S V T L
      TGTGCCGAGTCCCCCTGGATTGTGTTCTGTATCGATATGGTTCCCTTTCCGTACACCTG
361 -----!-----!-----!-----!-----!-----! 420

      D I V Q G   W G Q G T T V T V S S A S T K
      GACATTGTCCAGGGTTGGGGCCAAGGAACCACGGTCACCGTCTCCAGCGCTCCACCAAG
421 -----!-----!-----!-----!-----!-----! 480

      G P S V F P L A P S S K S T S G G T A A
      GGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
481 -----!-----!-----!-----!-----!-----! 540

      L G C I V K D Y F P E P V T V S W N S G
      CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGC
541 -----!-----!-----!-----!-----!-----! 600

      A L T S G V H T F P A V L Q S S G L Y S
      GCCCTGACCAGCGGCGTGCACACCTT'CCCGGCTGTCTTACAGTCC'CCAGGACTCTACTCC
601 -----!-----!-----!-----!-----!-----! 660

      L S S V V T V P S S S L G T Q T Y I C N
      CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC
661 -----!-----!-----!-----!-----!-----! 720

      V N H K P S N T K V D K K V E P K S C D
      GTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
721 -----!-----!-----!-----!-----!-----! 780

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64/121

Figure 30 continued

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      K T H T C P P C P A P E L L G G P S V F
      AAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
781 -----!-----!-----!-----!-----!-----! 840

      L F P P K P K D T L M I S R T P E V T C
      CTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGC
841 -----!-----!-----!-----!-----!-----! 900

      V V V D V S H E D P E V K F N W Y V D G
      GTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
901 -----!-----!-----!-----!-----!-----! 960

      V E V H N A K T K P R E E Q Y N S T Y R
      GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
961 -----!-----!-----!-----!-----!-----! 1020

      V V S V L T V L H Q D W L N G K E Y K C
      GTGGTCAGCGTCCTCACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
1021 -----!-----!-----!-----!-----!-----! 1080

      K V S N K A L P A P I E K T I S K A K G
      AAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGG
1081 -----!-----!-----!-----!-----!-----! 1140

      Q P R E P Q V Y T L P P S R D E L T K N
      CAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAAC
1141 -----!-----!-----!-----!-----!-----! 1200

      Q V S I L T C L V K G F Y P S D I A V E W
      CAGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGG
1201 -----!-----!-----!-----!-----!-----! 1260

      E S N G Q P E N N Y K T T P P V L D S D
      GAGAGCAATGGGAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGAC
1261 -----!-----!-----!-----!-----!-----! 1320

      G S F F L Y S K L T V D K S R W Q Q G N
      GGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
1321 -----!-----!-----!-----!-----!-----! 1380

      V F S C S V M H E A L H N H Y T Q K S L
      GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
1381 -----!-----!-----!-----!-----!-----! 1440

      S L S P G K *
      TCCCTGTCTCCGGGTAAATGATCTAAAGGGCGAATTCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----!-----! 1495
```

B: Light Variable + Human kappa constant (SEQ ID NO: 102)

```
      BamHI      M G W S C I I L F L V A T A T G V
      GGATCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

      H S D V L M T Q S P L S L P V T P G E P
      CACTCCGATGTGTTGATGACCAATCTCCACTCTCCCTGCCTGTCACTCCTGGGGAGCCA
61 -----!-----!-----!-----!-----!-----! 120
```

SUBSTITUTE SHEET (RULE 26)

Figure 30 continued

```

      A S I S C W N R Q L Y P E W T E A Q R L
121 GCCTCGATCTCTTGCTGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCCAGAGACTT 180
      -----!-----!-----!-----!-----!-----!-----!

      D W Y L Q K P G Q S P Q L L I Y A N C S
181 GACTGGTATCTGCAGAAACCAGGCCAGTCTCCACAGCTCCTGATCTACGCCAACTGCAGT 240
      -----!-----!-----!-----!-----!-----!-----!

      V Y D F F V W L H Y Y S V R D T L L G P
241 GTTTATGATTTTGTGTGGCTCCATTATTATCTGTAGAGATACATTATTAGGACCA 300
      -----!-----!-----!-----!-----!-----!-----!

      G R P Y R G V P D R F S G S G S G T D F
301 GGACGCCCCCTACAGGGGGGTCCCAGACAGATTCACTGGCAGTGGATCAGGGACAGATTTC 360
      -----!-----!-----!-----!-----!-----!-----!

      T L K I S R V E A E D T G V Y Y C Q C T
361 ACACCTCAAGATCAGCAGAGTGGAGGCTGAGGATACCGAGTGTATTACTGCCAGTGCACA 420
      -----!-----!-----!-----!-----!-----!-----!

      E V R A D T R P W S G P Y I L R N Q D D
421 GAGGTGCGAGCCGACACAAGGCCCTGGAGTGGTCCCTACATCCTACGAAACCAGGATGAC 480
      -----!-----!-----!-----!-----!-----!-----!

      R E L W P R K F F F G G G T K V E I K R
481 CGTGAGCTGTGGCCAAGAAAATTCTTCTTCGGTGGAGGCACCAAGGTGGAATCAAGCGT 540
      -----!-----!-----!-----!-----!-----!-----!

      T V A A P S V F I F P P S D E Q L K S G
541 ACGGTAGCGGCCCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 600
      -----!-----!-----!-----!-----!-----!-----!

      T A S V V C L L N N F Y P R E A K V Q W
601 ACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG 660
      -----!-----!-----!-----!-----!-----!-----!

      K V D N A L Q S G N S Q E S V T E Q D S
661 AAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGC 720
      -----!-----!-----!-----!-----!-----!-----!

      K D S T Y S L S S T L T L S K A D Y E K
721 AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAA 780
      -----!-----!-----!-----!-----!-----!-----!

      H K V Y A C E V T H Q G L S S P V T K S
781 CACAAAGTCTACGCCCTGCGAAGTCAACCCAGGGCCTGAGCTCGCCCGTCAACAAAGAGC 840
      -----!-----!-----!-----!-----!-----!-----!

1: F N R G E C * XhoI
TTCAACAGGGGAGAGTGTGACTCGAG
841 -----!-----!-----!-----!-----!-----!-----! 867

```

Figure 31: Sequence of pVAXDCIB238 iV1(iCIB1plus)

A: Heavy Variable + HuigG1 CH1-Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO:2)

```

HindIII M G W S C I I L F L V A T A T G V
1 AAGCTTACCATGGGATGGAGCTGTATCATTCCTCTTCTTGGTAGCAACAGTACCGGAGTC 60
      -----!-----!-----!-----!-----!-----!-----!

```

66/121

Figure 31 continued

```

H S Q V Q L V E T G G G L I Q P G G S L
CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTG
61 -----!-----!-----!-----!-----!-----!-----! 120

R M S C G T G R A M L G T H T M E V T V
AGAATGTCTCTGCGGACAGGCAGGGCAATGCTGGGCACACACCATGGAAGTGACTGTC
121 -----!-----!-----!-----!-----!-----!-----! 180

Y H W V R Q A P G K G L E W I A Y I G S
TACCATTGGGTTTCGGCAGGCTCCGGGGAAGGGGCTGGAGTGGATCGCATACATTGGTAGT
181 -----!-----!-----!-----!-----!-----!-----! 240

G G S V Y D F F V W L R F T I S R D N S
GGTGGTAGTGTATTATGATTTTTTGTGTGGCTCCGATTACCATTTCCAGAGACAATAGC
241 -----!-----!-----!-----!-----!-----!-----! 300

K N T L Y L Q L N S L R A E D T A V Y Y
AAGAACACCCCTGTATTTGCAATTGAACAGTCTGAGGGCTGAGGACACAGCCGTGTATTAC
301 -----!-----!-----!-----!-----!-----!-----! 360

C A R V P L D C V L Y R Y G S F S V T L
TGTGCCCCGAGTCCCCCTGGATTGTGTTCTGTATCGATATGGTTCCCTTTCCGTCACCCTG
361 -----!-----!-----!-----!-----!-----!-----! 420

D I V Q G W G Q G T T V T V S S A S T K
GACATTGTCCAGGGTGGGGCCAAGGAACCACGGTCACCGTCTCCAGCGCTTCCACCAAG
421 -----!-----!-----!-----!-----!-----!-----! 480

G P S V F P L A P S S K S T S G G T A A
GGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
481 -----!-----!-----!-----!-----!-----!-----! 540

L G C L V K D Y F P E P V T V S W N S G
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC
541 -----!-----!-----!-----!-----!-----!-----! 600

A L T S G V H T F P A V L Q S S G L Y S
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCC
601 -----!-----!-----!-----!-----!-----!-----! 660

L S S V V T V P S S S L G T Q T Y I C N
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC
661 -----!-----!-----!-----!-----!-----!-----! 720

V N H K P S N T K V D K K V E P K S C D
GTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGTGAC
721 -----!-----!-----!-----!-----!-----!-----! 780

K T H T C P P C P A P E L L G G P S V F
AAAACACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
781 -----!-----!-----!-----!-----!-----!-----! 840

L F P P K P K D T L M I S R T P E V T C
CTCTTCCCCCAAACCAAGGACACCCATCATGATCTCCCGGACCCCTGAGGTCACATGC
841 -----!-----!-----!-----!-----!-----!-----! 900
```

SUBSTITUTE SHEET (RULE 26)

67/121

Figure 31 continued

V V V D V S H E D P E V K F N W Y V D G
GTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGC
901 -----!-----!-----!-----!-----!-----! 960

V E V H T A W T Q P R E E Q Y N S T Y R
GTGGAGGTGCATACAGCCTGGACACAGCCGGGAGGAGCAGTACAACAGCACGTACCGT
961 -----!-----!-----!-----!-----!-----! 1020

V V S V L T V L H Q D W L N G K E Y K C
GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
1021 -----!-----!-----!-----!-----!-----! 1080

K V S N K A L P A P I E K T I S K P K G
AAGGTCCTCAACAAAGCCCTCCCAGCCCCATCGAGAAACCATCTCAAACCCAAAGGG
1081 -----!-----!-----!-----!-----!-----! 1140

R A Q T P Q V Y T I P P P R E Q M S K K
AGAGCCCAGACACCACAGGTGTACACCATACCCCCACCTCGGGAACAAATGTCCAAGAAG
1141 -----!-----!-----!-----!-----!-----! 1200

K V S I T C L V T N F F S E A I S V E W
AAGGTCAGCCTGACCTGCCTGGTCACCAACTTCTTCTCTGAAGCCATCAGTGTGGAGTGG
1201 -----!-----!-----!-----!-----!-----! 1260

E S N G Q P E N N Y K T T P P V L D S D
GAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
1261 -----!-----!-----!-----!-----!-----! 1320

G S F F L Y S K L T V D K S R W Q Q G N
GGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
1321 -----!-----!-----!-----!-----!-----! 1380

V F S C S V M H E A L H N H Y T Q K S L
GTCTTCTCATGTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
1381 -----!-----!-----!-----!-----!-----! 1440

S L S P G K * EcoRI
TCCCTGTCTCCGGTAAATGATCTAAAGGGCGATATCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----!-----! 1495

B: Light Variable + Human kappa constant (SEQ ID NO: 10)

BamHI M G W S C I I L F L V A T A T G V
GGATCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

H S D V L M T Q S P L S L P V T P G E P
CACTCCGATGTGTGATGACCCAACTCTCCACTCTCCCTGCCTGTCACTCCTGGGGAGCCA
61 -----!-----!-----!-----!-----!-----! 120

A S I S C W N R Q L Y P E W T E A Q R L
GCCTCGATCTCTTGGTGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCCAGAGACTT
121 -----!-----!-----!-----!-----!-----! 180

D W Y L Q K P G Q S P Q L L I Y A N C S
GACTGGTATCTGCAGAAACCAGGCCAGTCTCCACAGCTCCTGATCTACGCCAACTGCAGT
181 -----!-----!-----!-----!-----!-----! 240

Figure 31 continued

```

V Y D F F V W L H Y Y S V R D T L L G P
241 GTTTATGATTTTTTTGTGTGGCTCCATTATTCTGTAGAGATACATTATTAGGACCA 300
-----!-----!-----!-----!-----!-----!

G R F Y R G V P D R F S G S G S G T D F
301 GGACGCCCTACAGGGGGTCCCAGACAGATTTCAGTGGCAGTGGATCAGGGACAGATTTCC
-----!-----!-----!-----!-----!-----!

T L K I S R V E A E D T G V Y Y C Q C T
361 AACTCAAGATCAGCAGAGTGGAGGCTGAGGATACCGAGTGTATTACTGCCAGTGCACA
-----!-----!-----!-----!-----!-----!

E V R A D T R P W S G P Y I L R N Q D D
421 GAGGTGCCGAGCCGACACAAGGCCCTGGAGTGGTCCCTACATCCTACGAAACCAGGATGAC
-----!-----!-----!-----!-----!-----!

R E L W P R K F F F G G G T K V E I K R BsiWI
481 CGTGAGCTGTGGCCAAGAAAATTCTTCTCGGTGGAGGCACCAAGGTGGAATCAAGCGT
-----!-----!-----!-----!-----!-----!

T V A A P S V F I F P P S D E Q L K S G
541 ACGGTAGCGGCCCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA
-----!-----!-----!-----!-----!-----!

T A S V V C L L N N F Y P R E A K V Q W
601 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
-----!-----!-----!-----!-----!-----!

K V D N A L Q S G N S Q E S V T E Q D S
661 AAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGC
-----!-----!-----!-----!-----!-----!

K D S T Y S L S S T L T L S K A D Y E K
721 AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAA
-----!-----!-----!-----!-----!-----!

H K V Y A C E V T H Q G L S S P V T K S
781 CACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
-----!-----!-----!-----!-----!-----!

1: F N R G E C * XhoI
TTCAACAGGGGAGAGTGTGACTCGAG
841 -----!-----!-----!-----!-----! 867

```

Figure 32: Sequence of pVAXDCIB178(SCIB2)

A: Heavy Variable + HuigG1 CH1-Hinge-CH2-CH3 (SEQ ID NO: 103)

```

HindIII M G W S C I I L F L V A T A T G V
AAGCTT AAGCTTACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

H S Q V Q L V E T G G G L I Q P G G S L
CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTG
61 -----!-----!-----!-----!-----!-----! 120

```

Figure 32 continued

```

      R M S C L L M W I T Q C F W V R Q A P G
AGAATGTCCTGCTGTTGATGTGGATCACGCAGTGTCTTTGGGTTCGGCAGGCTCCGGG
121 -----!-----!-----!-----!-----!-----! 180

      K G L E W I A Y I G S G G S L L M W I T
AAGGGGCTGGAGTGGATCGCATACATTGGTAGTGGTGGTTCCTTGTGATGTGGATCACG
181 -----!-----!-----!-----!-----!-----! 240

      Q C R F T I S R D N S K N T L Y L Q L N
CAGTGCCTGATTACCATTTCCAGAGACAATAGCAAGAACCCTGTATTTGCAATTGAAC
241 -----!-----!-----!-----!-----!-----! 300

      S L R A E D T A V Y Y C A R P E S R L L
AGTCTGAGGGCTGAGGACACAGCCGTGTATTACTGTGCCGACCGGAGAGCCGCCTGCTT
301 -----!-----!-----!-----!-----!-----! 360

      E F Y L A M P F A T P M E A E L A R R S
GAGTTCTACCTCGCCATGCCTTTTCGCGACACCCATGGAAGCAGAGCTGGCCCGCAGGAGC
361 -----!-----!-----!-----!-----!-----! 420

      L A Q W G Q G T T V T V S S A S T K G P
CTGGCCCACTGGGGCCAAGGAACCACGGTCACCGTCTCCAGCGCTTCCACCAAGGGCCA
421 -----!-----!-----!-----!-----!-----! 480

      S V F P L A P S S K S T S G G T A A L G
TCCGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGC
481 -----!-----!-----!-----!-----!-----! 540

      C L V K D Y F P E P V T V S W N S G A L
TGCTTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTG
541 -----!-----!-----!-----!-----!-----! 600

      T S G V H T F P A V L Q S S G L Y S L S
ACCAGCGGCGTGACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC
601 -----!-----!-----!-----!-----!-----! 660

      S V V T V P S S S L G T Q T Y I C N V N
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
661 -----!-----!-----!-----!-----!-----! 720

      H K P S N T K V D K K V E P K S C D K T
CACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAC
721 -----!-----!-----!-----!-----!-----! 780

      H T C P P C P A P E L L G G P S V F L F
CACACATGCCCACCGTGCCCGAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTC
781 -----!-----!-----!-----!-----!-----! 840

      P P K P K D T L M I S R T P E V T C V V
CCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG
841 -----!-----!-----!-----!-----!-----! 900

```

Figure 32 continued

```
V D V S H E D P E V K F N W Y V D G V E
GTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
901 -----!-----!-----!-----!-----!-----! 960

V H N A K T K P R E E Q Y N S T Y R V V
GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
961 -----!-----!-----!-----!-----!-----! 1020

S V L T V L H Q D W L N G K E Y K C K V
AGCGTCTTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC
1021 -----!-----!-----!-----!-----!-----! 1080

S N K A L P A P I E K T I S K A K G Q P
TCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
1081 -----!-----!-----!-----!-----!-----! 1140

R E P Q V Y T L P P S R D E L T K N Q V
CGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTC
1141 -----!-----!-----!-----!-----!-----! 1200

S L T C L V K G F Y P S D I A V E W E S
AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGC
1201 -----!-----!-----!-----!-----!-----! 1260

N G Q P E N N Y K T T P P V L D S D G S
AATGGGCGAGCCGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCC
1261 -----!-----!-----!-----!-----!-----! 1320

F F L Y S K L T V D K S R W Q Q G N V F
TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
1321 -----!-----!-----!-----!-----!-----! 1380

S C S V M H E A L H N H Y T Q K S L S L
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
1381 -----!-----!-----!-----!-----!-----! 1440

S P G K *
TCTCCGGGTAAATGATCTAAAGGGCGAATTCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----!-----! 1489
```

B: Light Variable + Human kappa constant (SEQ ID NO: 11)

```
BamHI M G W S C I I L F L V A T A T G V
GGATCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

H S D V L M T Q S P L S L P V T P G E P
CACTCCGATGTGTGATGACCAATCTCCACTCTCCCTGCCTGTCACTCCTGGGGAGCCA
61 -----!-----!-----!-----!-----!-----! 120

A S I S C P G V L L K E F T V S G N I L
GCCTCGATCTCTTGCCAGGGGTGCTTCTGAAGGAGTTCAGTGTGTCGGCAACATACTG
121 -----!-----!-----!-----!-----!-----! 180

T I R L T A A D H R W Y L Q K P G Q S P
ACTATCCGACTGACTGCTGCAGACCACCGCTGGTATCTGCAGAAACCAGGCCAGTCTCCA
181 -----!-----!-----!-----!-----!-----! 240
```

Figure 32 continued

```

      Q L L I Y K V S N R F S G V P D R F S G
      CAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGATTCAGTGGC
241 -----!-----!-----!-----!-----!-----! 300

      S G S G T D F T L K I S R V E A E D T G
      AGTGGATCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATACCGGA
301 -----!-----!-----!-----!-----!-----! 360

      V Y Y C F Q G S H V P W T F G G G T K V
      GTGTATTACTGCTTTCAAGGTTACATGTTCCGTGGACGTTCCGTGGAGGCACCAAGGTG
361 -----!-----!-----!-----!-----!-----! 420

      BsiWI
      E I K R T V A A P S V F I F P P S D E Q
      GAAATCAAGCGTACGGTAGCGGCCCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAG
421 -----!-----!-----!-----!-----!-----! 480

      L K S G T A S V V C L L N N F Y P R E A
      TTGAAATCTGGAAGTGCCTCTGTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCC
481 -----!-----!-----!-----!-----!-----! 540

      K V Q W K V D N A L Q S G N S Q E S V T
      AAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACACA
541 -----!-----!-----!-----!-----!-----! 600

      E Q D S K D S T Y S L S S T L T L S K A
      GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA
601 -----!-----!-----!-----!-----!-----! 660

      D Y E K H K V Y A C E V T H Q G L S S P
      GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCC
661 -----!-----!-----!-----!-----!-----! 720

      V T K S F N R G E C * XhoI
      GTCACAAAGAGCTTCAACAGGGGAGAGTGTGACTCGAG
721 -----!-----!-----!-----!-----!-----! 759

```

Figure 33: Sequence of pVAXDCIB178 iV1 (iSCIB2)

A: Heavy Variable + HuigG1 CH1-Hinge-CH2-CH3 iV1 (murine igG3 23 AA substitutions in bold) (SEQ ID NO:3)

```

      HindIII M G W S C I I L F L V A T A T G V
      AAGCTTACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

      H S Q V Q L V E T G G G L I Q P G G S L
      CACTCCCAGGTGCAGCTGGTGGAGACTGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTG
61 -----!-----!-----!-----!-----!-----! 120

      R M S C L L M W I T Q C F W V R Q A P G
      AGAATGTCCTGCTGTTGATGTGGATCACGCAGTGCTTTTGGGTTTCGGCAGGCTCCGGGG
121 -----!-----!-----!-----!-----!-----! 180

      K G L E W I A Y I G S G G S L L M W I T
      AAGGGGCTGGAGTGGATCGCATACATTGGTAGTGGTGGTTCCTGTTGATGTGGATCACG
181 -----!-----!-----!-----!-----!-----! 240

```

Figure 33 continued

241 Q C R F T I S R D N S K N T L Y L Q L N
CAGTGC CGATTTCACCATTTCCAGAGACAATAGCAAGAACACCCTGTATTTGCAATTGAAC
-----!-----!-----!-----!-----!-----!-----! 300

301 S L R A E D T A V Y Y C A R P E S R L L
AGTCTGAGGGCTGAGGACACAGCCGTGTATTACTGTGCCCAGCCGGAGAGCCGCCTGCTT
-----!-----!-----!-----!-----!-----!-----! 360

361 E F Y L A M P F A T P M E A E L A R R S
GAGTTCTACCTCGCCATGCCTTTTCGCGACACCCATGGAAGCAGAGCTGGCCCGCAGGAGC
-----!-----!-----!-----!-----!-----!-----! 420

AfeI

421 L A Q W G Q G T T V T V S S A S T K G P
CTGGCCCACTGGGGCCAAGGAACCACGGTCACCGTCTCCAGCGCTTCCACCAAGGGCCCA
-----!-----!-----!-----!-----!-----!-----! 480

481 S V F P L A P S S K S T S G G T A A L G
TCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGC
-----!-----!-----!-----!-----!-----!-----! 540

541 C L V K D Y F P E P V T V S W N S G A L
TGCTTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTG
-----!-----!-----!-----!-----!-----!-----! 600

601 T S G V H T F P A V L Q S S G L Y S L S
ACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCTCAGACTCTACTCCCTCAGC
-----!-----!-----!-----!-----!-----!-----! 660

661 S V V T V P S S S L G T Q T Y I C N V N
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGGACCCAGACCTACATCTGCAACGTGAAT
-----!-----!-----!-----!-----!-----!-----! 720

721 H K P S N T K V D K K V E P K S C D K T
CACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGTGACAAAAC
-----!-----!-----!-----!-----!-----!-----! 780

781 H T C P P C P A P E L L G G P S V F L F
CACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTC
-----!-----!-----!-----!-----!-----!-----! 840

841 P P K P K D T L M I S R T P E V T C V V
CCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTG
-----!-----!-----!-----!-----!-----!-----! 900

901 V D V S H E D P E V K F N W Y V D G V E
GTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG
-----!-----!-----!-----!-----!-----!-----! 960

961 V H T A W T Q P R E E Q Y N S T Y R V V
GTGCATACAGCCTGGACACAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
-----!-----!-----!-----!-----!-----!-----! 1020

1021 S V L T V L H Q D W L N G K E Y K C K V
AGCGTCTCACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC
-----!-----!-----!-----!-----!-----!-----! 1080

Figure 33 continued

S N K A L P A P I E K T I S K P K G R A
TCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAACCCAAAGGGAGAGCC
1081 -----!-----!-----!-----!-----!-----! 1140

Q T P Q V Y T I P P P R E Q M S K K K V
CAGACACCACAGGTGTACACCATACCCCCACCTCGGGAACAAATGTCCAAGAAGAAGGTC
1141 -----!-----!-----!-----!-----!-----! 1200

S L T C L V T N F F S E A I S V E W E S
AGCCTGACCTGCCTGGTCACCAACTTCTTCTCTGAAGCCATCAGTGTGGAGTGGGAGAGC
1201 -----!-----!-----!-----!-----!-----! 1260

N G Q P E N N Y K T T P P V L D S D G S
AATGGGACGCGGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCC
1261 -----!-----!-----!-----!-----!-----! 1320

F F L Y S K L T V D K S R W Q Q G N V F
TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
1321 -----!-----!-----!-----!-----!-----! 1380

S C S V M H E A L H N H Y T Q K S L S L
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
1381 -----!-----!-----!-----!-----!-----! 1440

S P G K * EcoRI
TCTCCGGGTAAATGATCTAAAGGGCGATATCGCCCTTAAGGGCGAATTC
1441 -----!-----!-----!-----!-----!-----! 1489

B: Light Variable + Human kappa constant (SEQ ID NO: 11)

BamHI M G W S C I I L F L V A T A T G V
GGATCCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACCGGAGTC
1 -----!-----!-----!-----!-----!-----! 60

H S D V L M T Q S P L S L P V T P G E P
CACTCCGATGTGTGATGACCAATCTCCACTCTCCCTGCCTGTCACTCTGGGGAGCCA
61 -----!-----!-----!-----!-----!-----! 120

A S I S C P G V L L K E F T V S G N I L
GCCTCGATCTCTTGCCAGGGGTGCTTCTGAAGGAGTTCACTGTGTCCGGCAACATACTG
121 -----!-----!-----!-----!-----!-----! 180

T I R L T A A D H R W Y L Q K P G Q S P
ACTATCCGACTGACTGCTGCAGACCACCGCTGGTATCTGCAGAAACCAGGCCAGTCTCCA
181 -----!-----!-----!-----!-----!-----! 240

Q L L I Y K V S N R F S G V P D R F S G
CAGCTCCTGATCTACAAAGTTTCCAACCGATTTCTGGGGTCCCAGACAGATTCAGTGGC
241 -----!-----!-----!-----!-----!-----! 300

S G S G T D F T L K I S R V E A E D T G
AGTGGATCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATACCGGA
301 -----!-----!-----!-----!-----!-----! 360

V Y Y C F Q G S H V P W T F G G G T K V
GTGTATTACTGCTTTCAAGGTTACATGTTCCGTGGACGTTCCGTGGAGGCACCAAGGTG
361 -----!-----!-----!-----!-----!-----! 420

Figure 33 continued

BsiWI
E I K R T V A A P S V F I F P P S D E Q
GAAATCAAG**CGTACG**GTAGCGGCCCATCTGTCTTCATCTTCCGCCATCTGATGAGCAG
421 -----!-----!-----!-----!-----!-----! 480

L K S G T A S V V C L L N N F Y P R E A
TTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC
481 -----!-----!-----!-----!-----!-----! 540

K V Q W K V D N A L Q S G N S Q E S V T
AAAGTACAGTGGAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCAACA
541 -----!-----!-----!-----!-----!-----! 600

E Q D S K D S T Y S L S S T L T L S K A
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA
601 -----!-----!-----!-----!-----!-----! 660

D Y E K H K V Y A C E V T H Q G L S S P
GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCC
661 -----!-----!-----!-----!-----!-----! 720

V T K S F N R G E C * **XhoI**
GTCACAAAGAGCTTCAACAGGGGAGAGTGTG**ACTCGAG**
721 -----!-----!-----!-----!-----! 759

Figure 34.

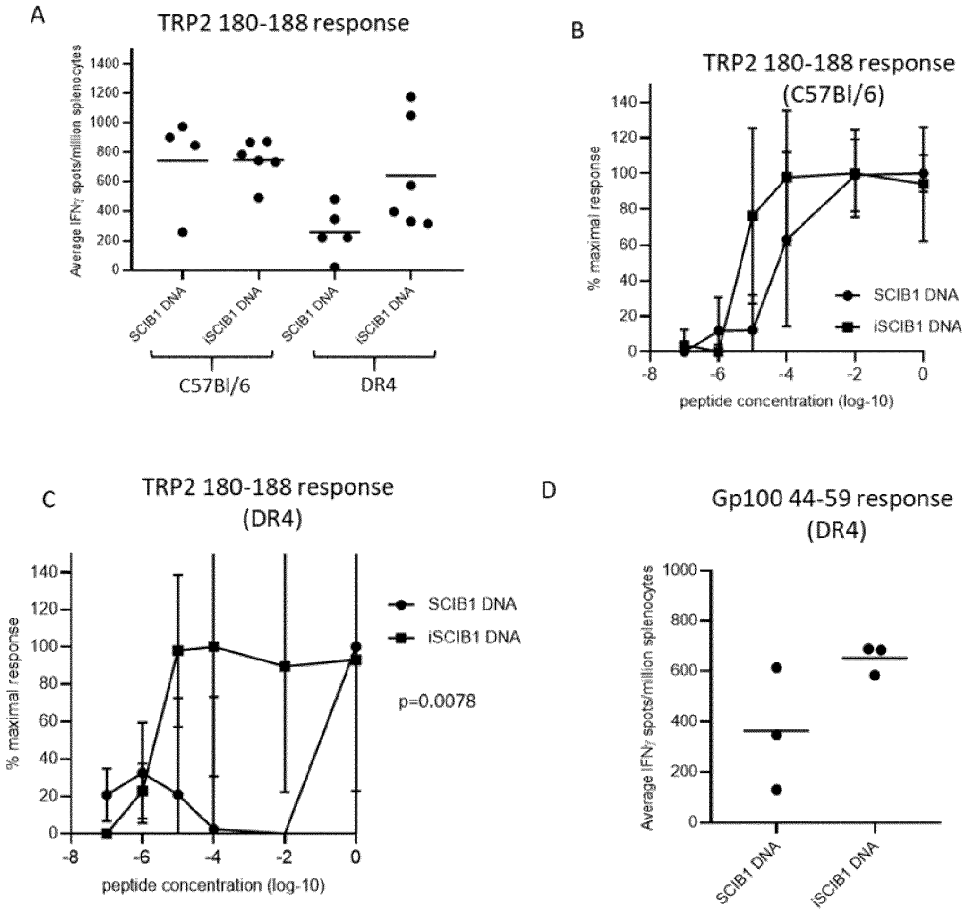


Figure 35.

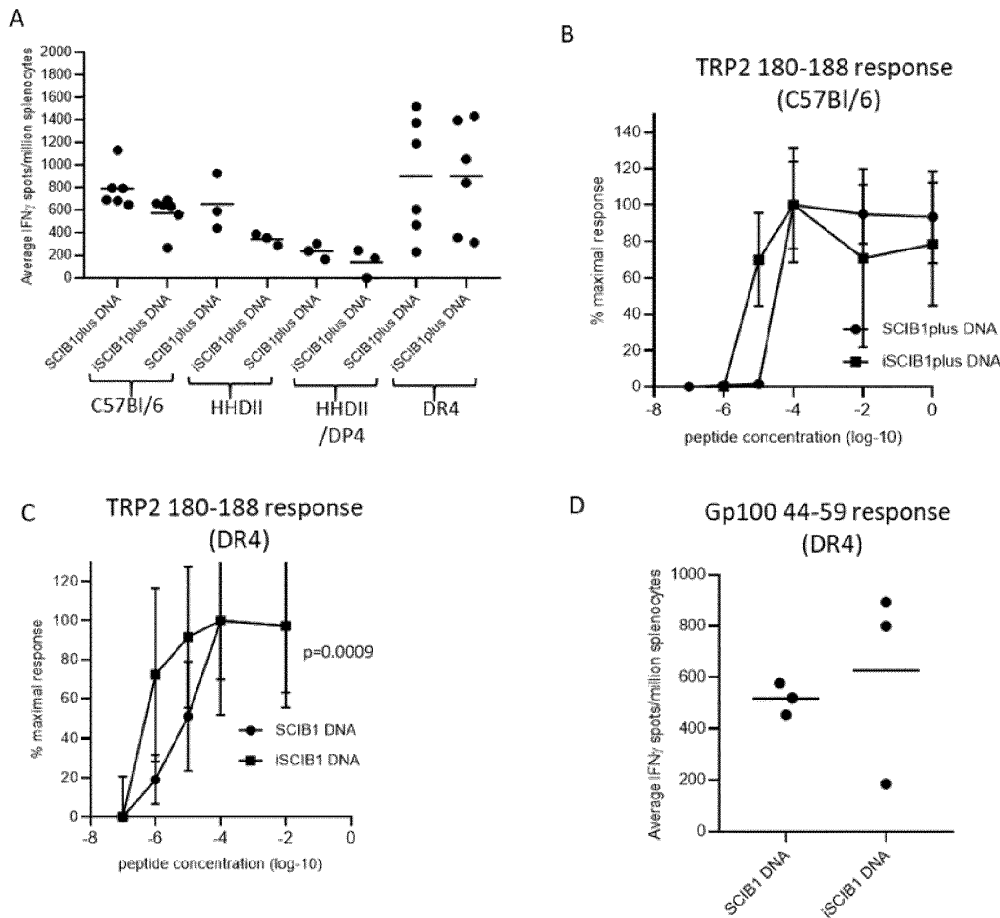


Figure 36.

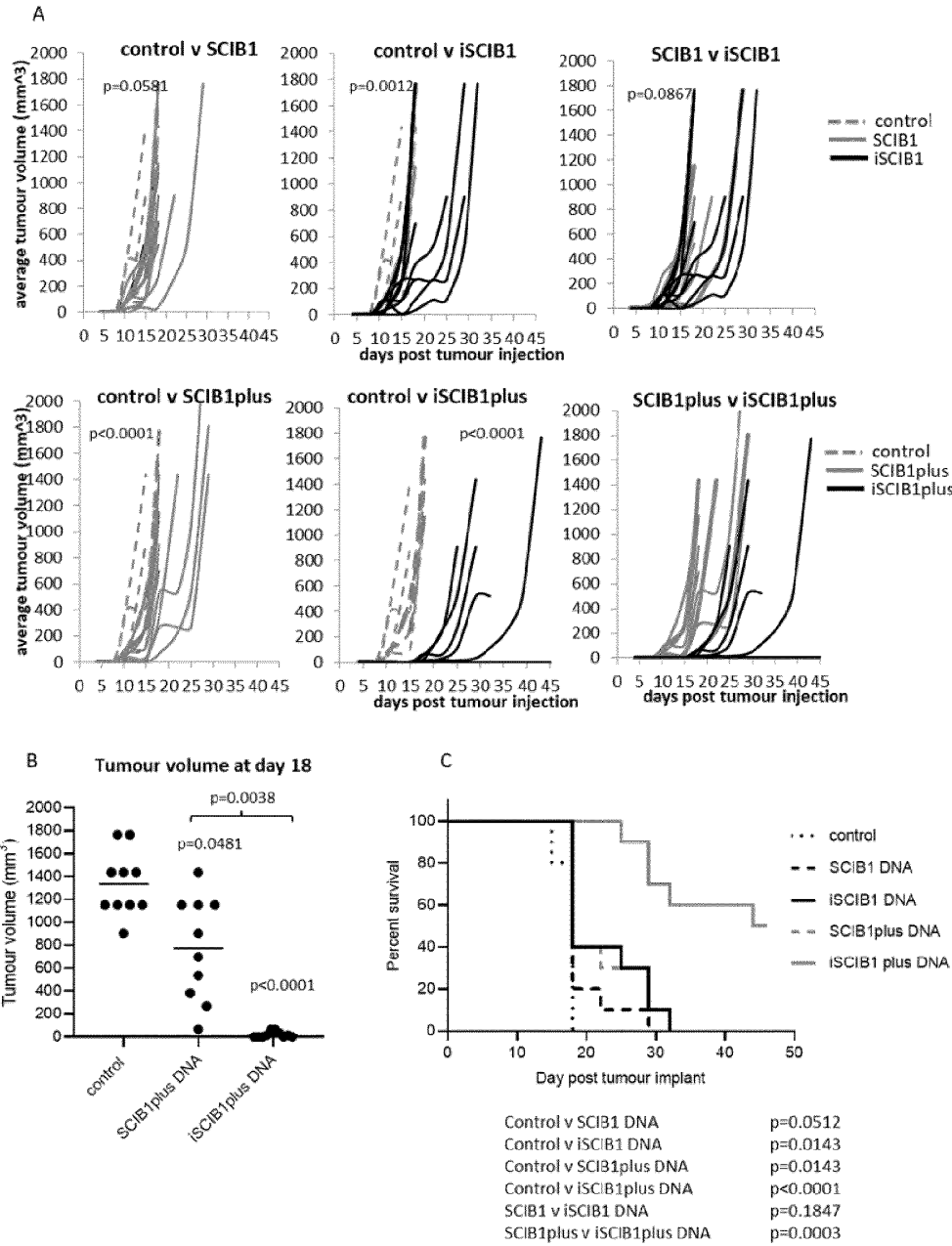


Figure 37.

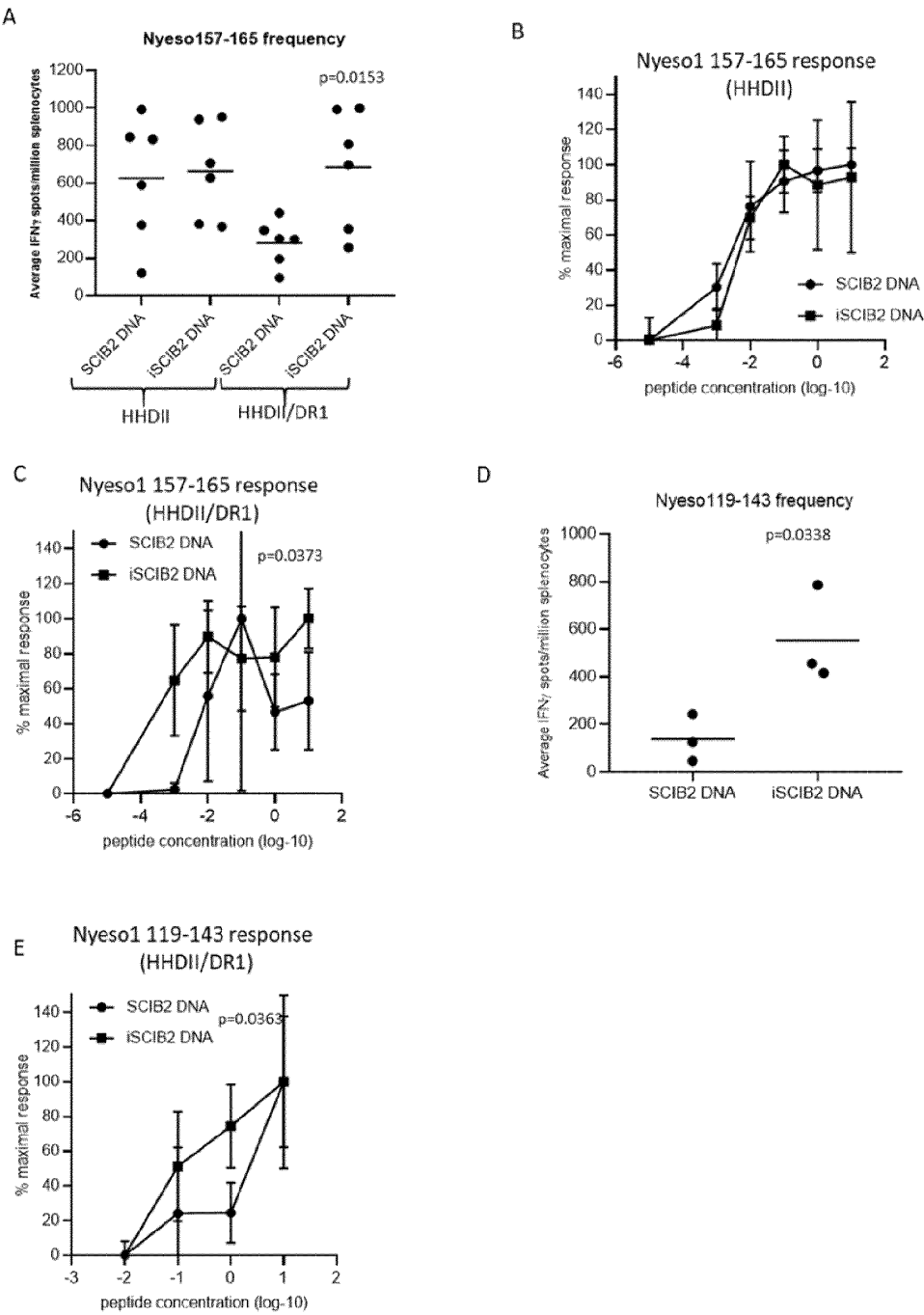


Figure 38.

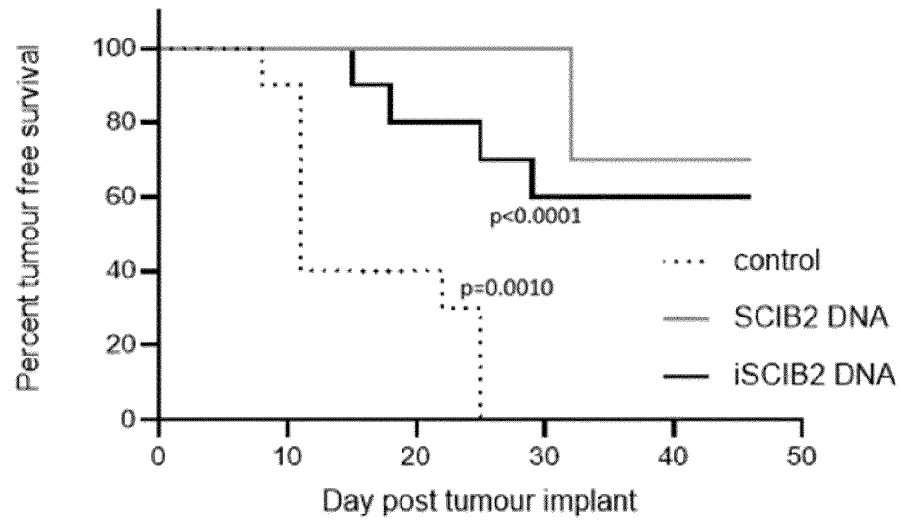


Figure 39.

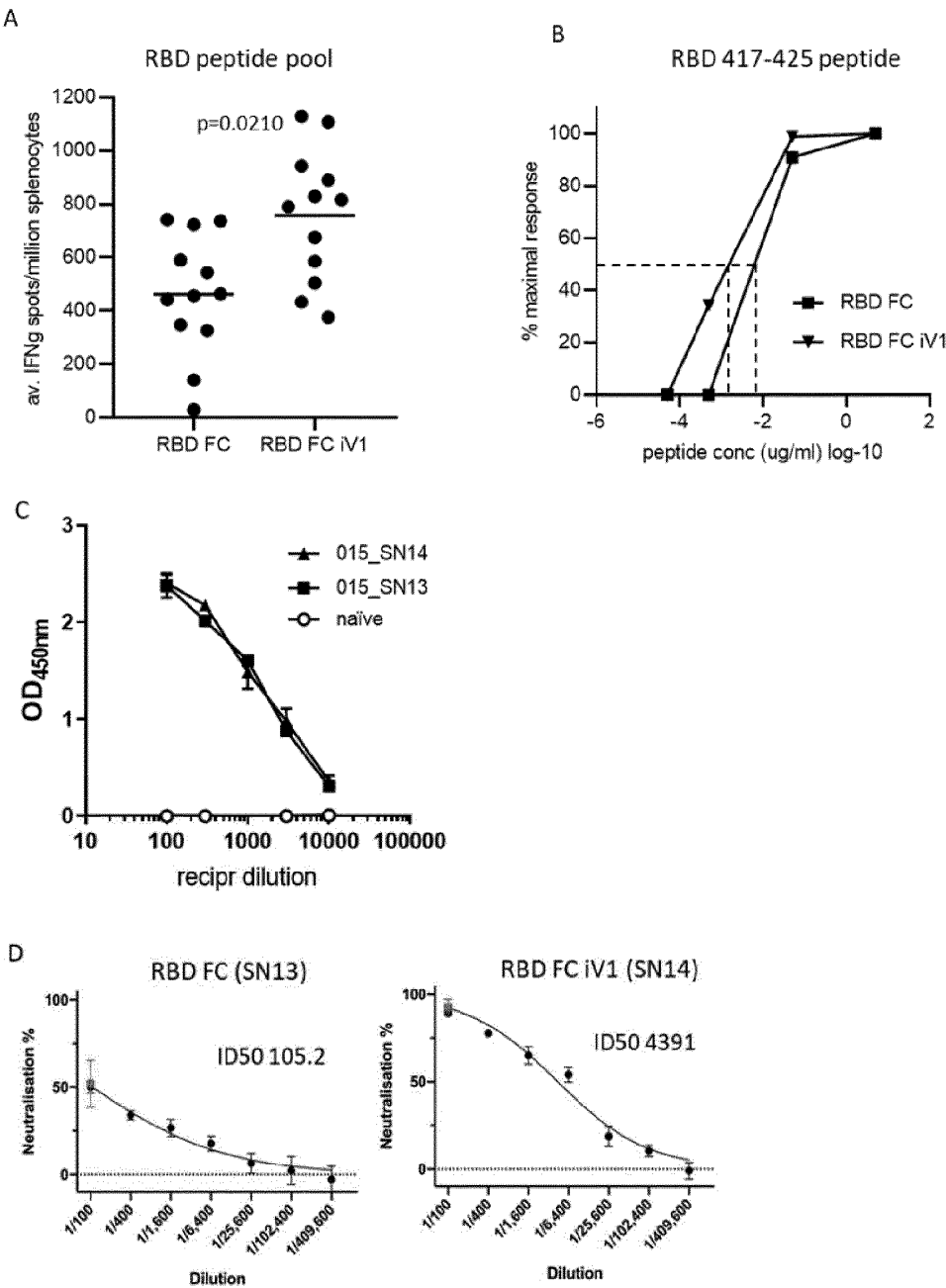


Figure 40.

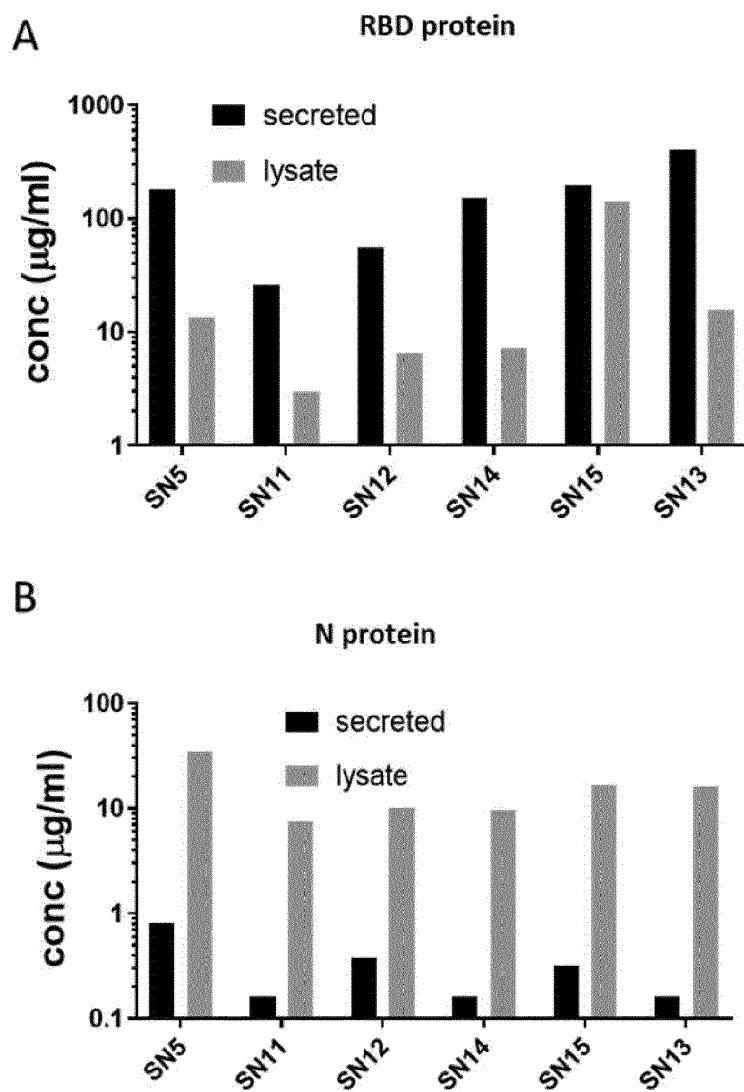


Figure 41.

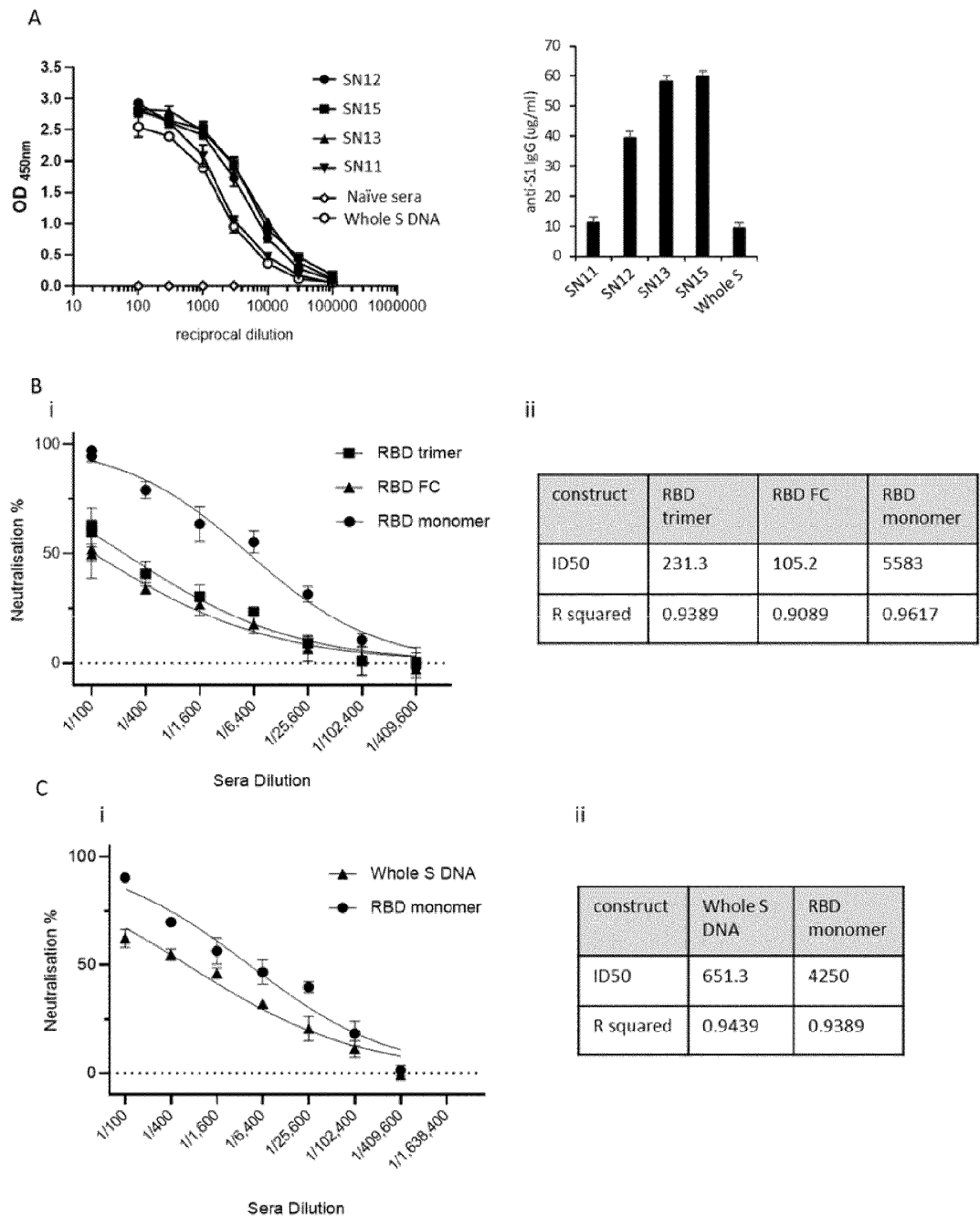


Figure 42.

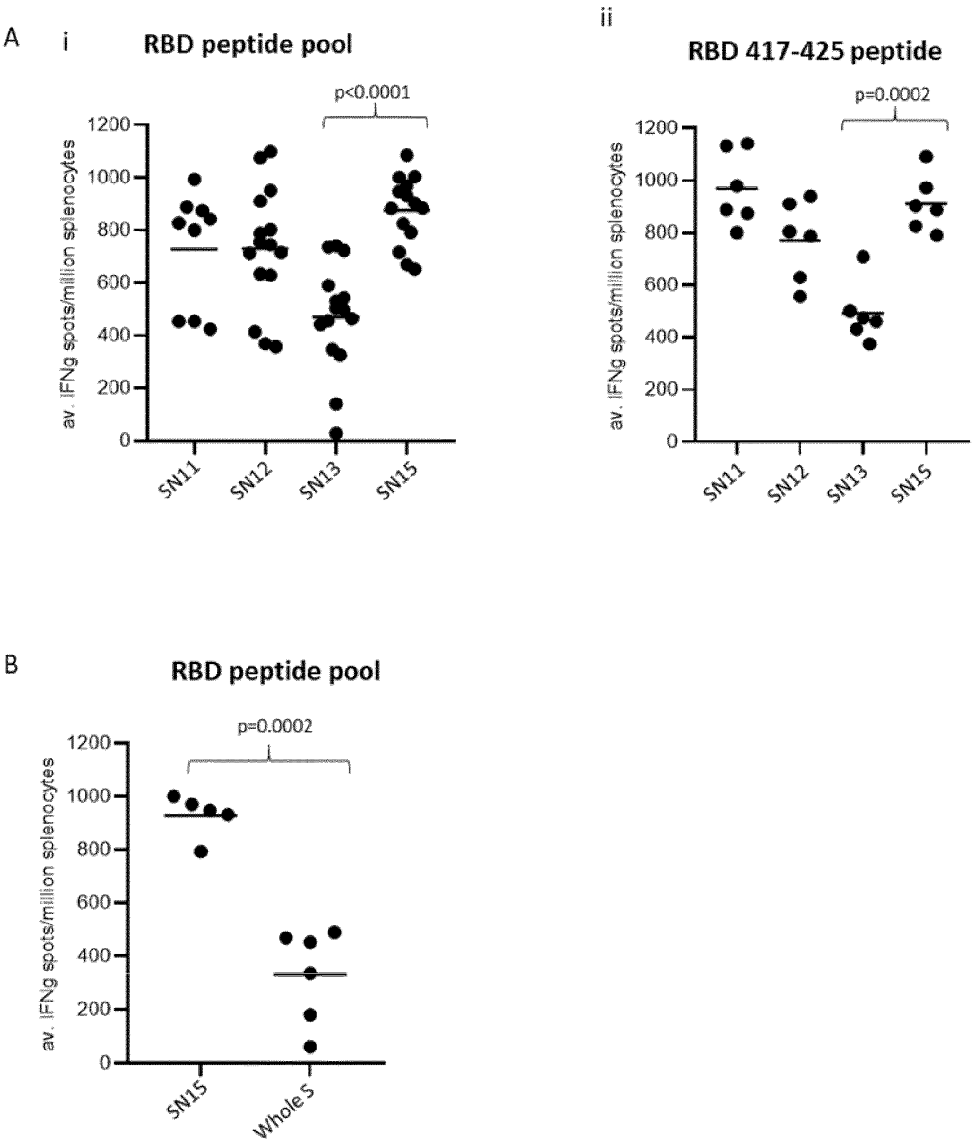


Figure 43.

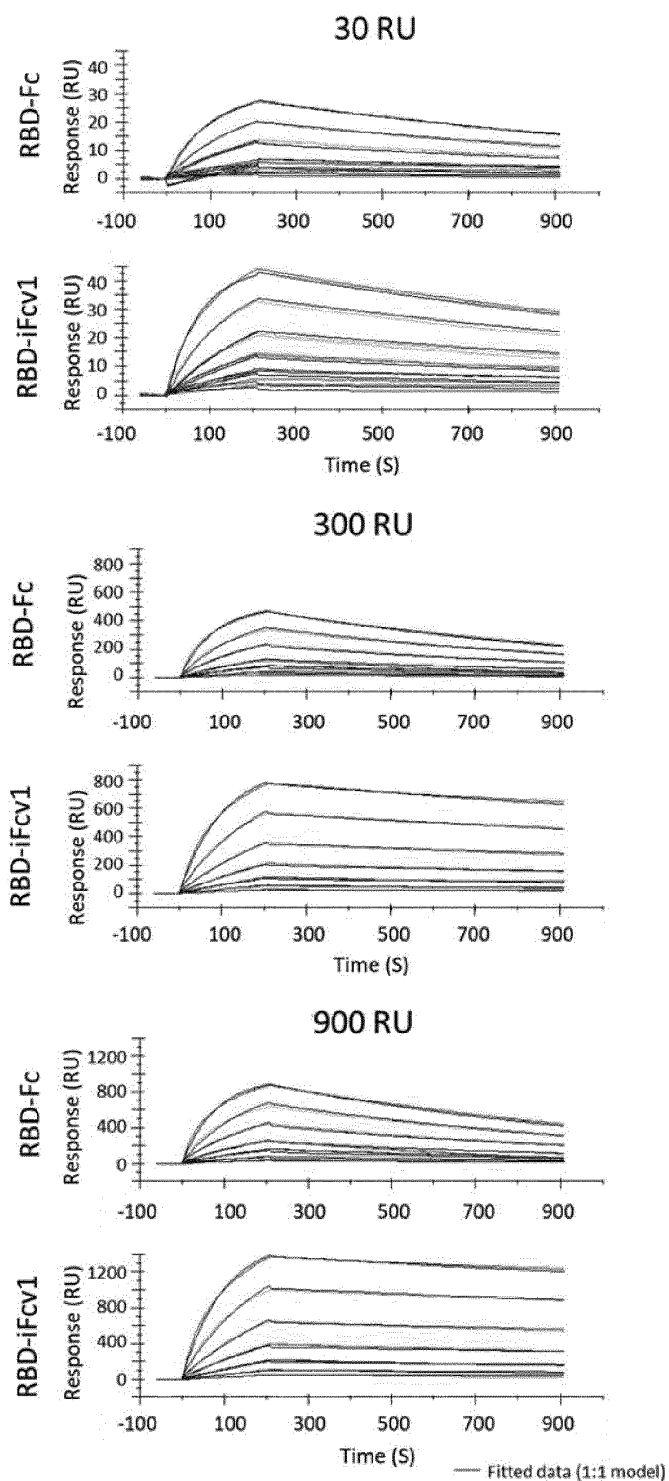
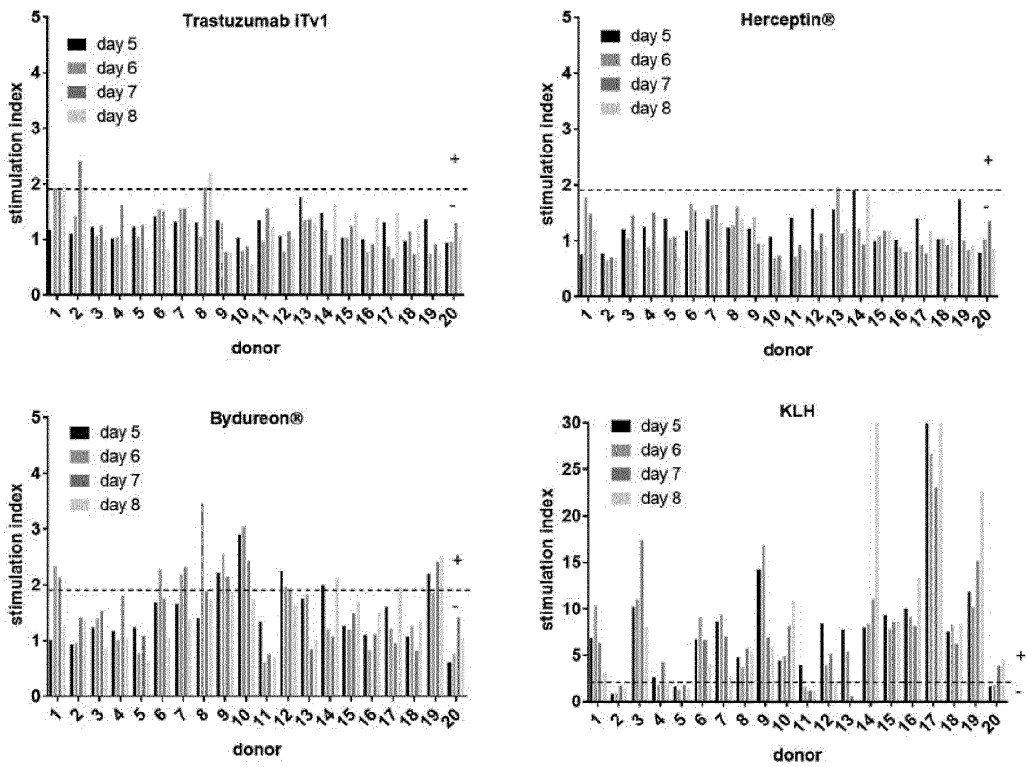


Figure 44.

A.



B.

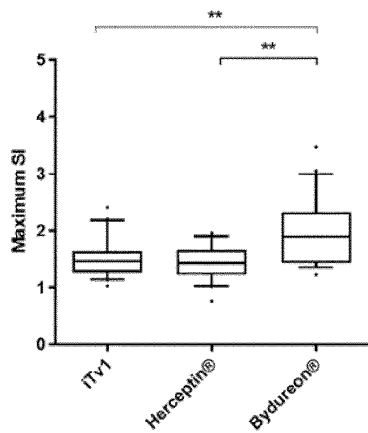


Figure 45.

A

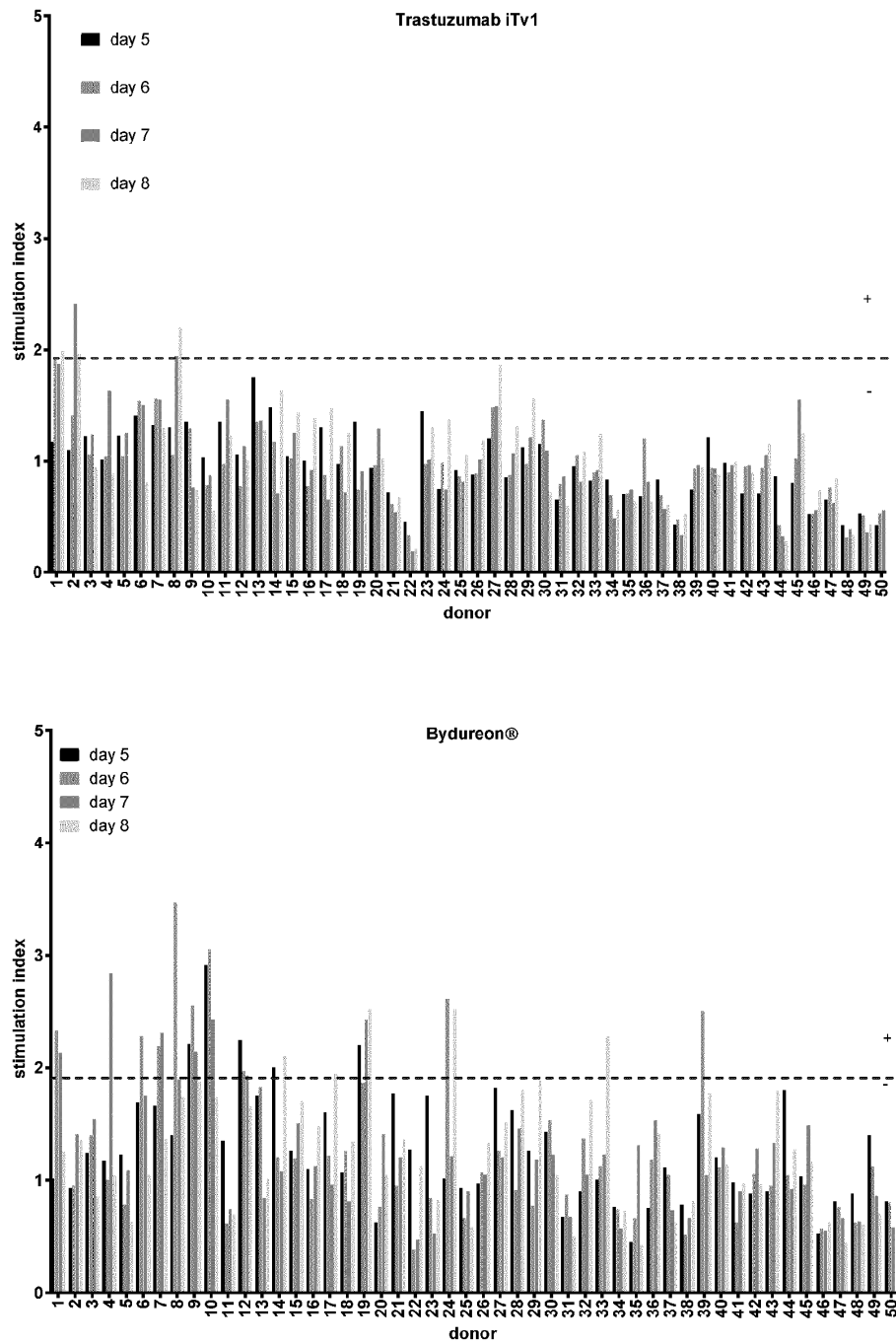


Figure 45.

A continued

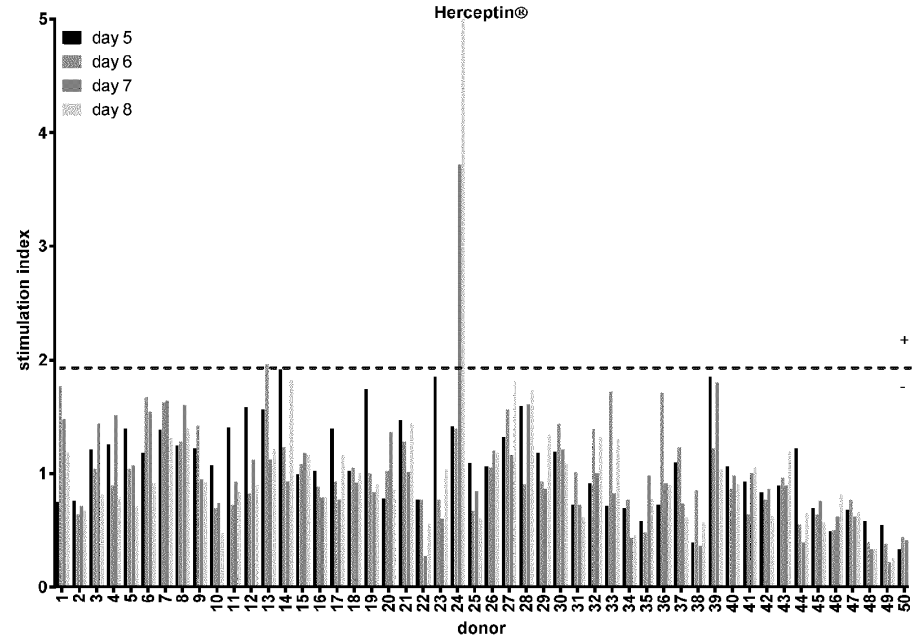
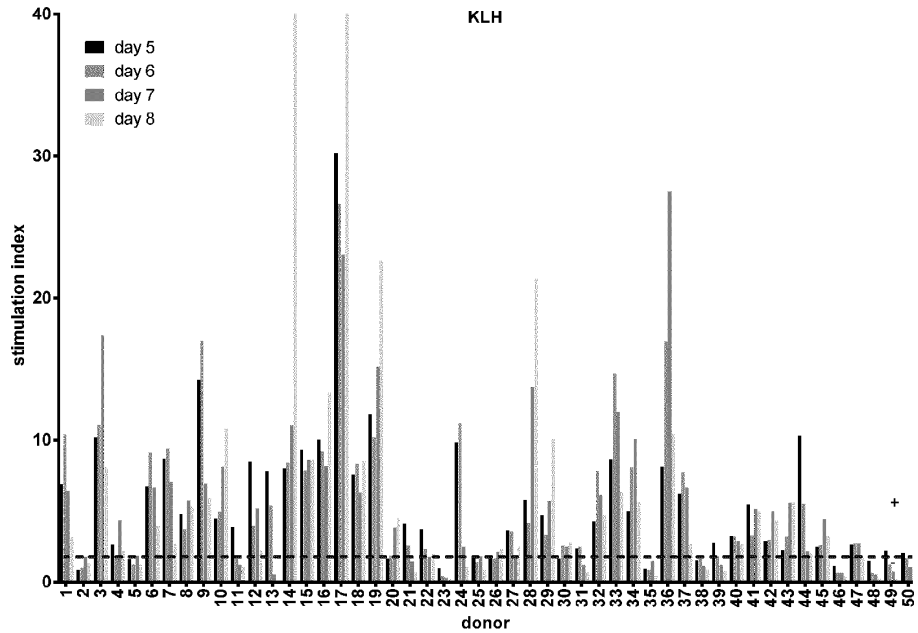


Figure 45.

B

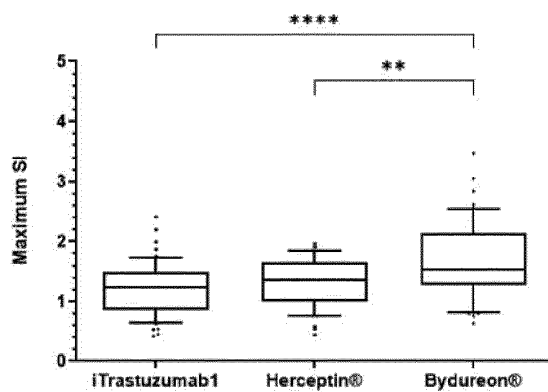
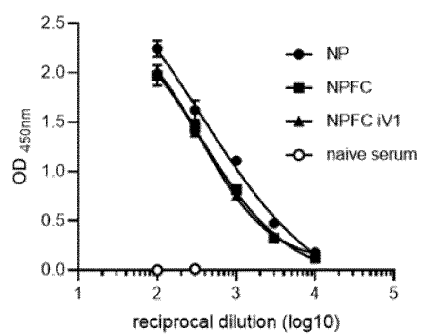


Figure 46.



	NP	NPFC	NPFC iV1
EC ₅₀	367	465	297
R squared	0.9907	0.9951	0.9986

Figure 47: Sequence of pVAXDCSN16; SN16

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) mut B1:1:7 (SEQ ID NO: 104)

BamHI M D W I W R I L F L V G A A T G
GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

A H S R V Q P T E S I V R F P N I T N L
GCACACAGCAGAGTGCAGCCACCGAGAGCATCGTGAGATTCCTCAACAATCACCAACCTG
61 -----!-----!-----!-----!-----!-----! 120

C P F G E V F N A T R F A S V Y A W N R
TGCCCCCTTCGGCGAGGTGTTCAACGCCACCAGATTGCGCAGCGGTGTACGCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180

K R I S N C V A D Y S V L Y N S A S F S
AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240

T F K C Y G V S P T K L N D L C F T N V
ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300

Y A D S F V I R G D E V R Q I A P G Q T
TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360

G K I A D Y N Y K L P D D F T G C V I A
GGCAAGATCGCCGACTACAACCTACAAGTGGCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420

W N S N N L D S K V G G N Y N Y L Y R L
TGGAACAGCAATAACCTGGACAGCAAGTGGGCGGCAACTACAACCTACCTTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480

F R K S N L K P F E R D I S T E I Y Q A
TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540

G S T P C N G V E G F N C Y F P L Q S Y
GGCAGCAGCCCCCTGCAACGGCGTGGAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----!-----! 600

N501Y MUTATION
G F Q P T **Y** G V G Y Q P Y R V V V L S F
GGCTTCCAGCCACCTACGGCGTGGGCTACCAGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----!-----! 660

E L L H A P A T V C G P K K S T N L V K
GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCCAAGAAGAGACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----!-----! 720

N K C V N F * **XhoI**
AACAAGTGGGTGAACCTTCTGATGACTCGAG
721 -----!-----!-----!-----! 750

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 IV1 mut B1:1:7 (murine igG3 23 AA substitutions in bold) (SEQ ID NO: 26)

HindIII M D W I W R I L F L V G A A T G
AAGCTTGGCCACCATGGACTGGATTGGAGAATCCTCTTCTGGTGGGAGCTGCCACAGGC

Figure 47 continued

1 -----!-----!-----!-----!-----!-----! 60
 D3L MUTATION
 A H S S **L** N G P Q N Q R N A P R I T F G
GCACACAGCAGCCTGAACGGGCCCCAGAACAGAGAAACGCCCCAGAATCACCTTCGGC
61 -----!-----!-----!-----!-----!-----! 120

 G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCAGCAACCAGAACGGCGAGAGAAGCGGCGCCAGAAGCAAG
121 -----!-----!-----!-----!-----!-----! 180

 Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACCGCCAGCTGGTTACCGCCCTGACCCAG
181 -----!-----!-----!-----!-----!-----! 240

 H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCTCCAGAGGCCAGGGCGTGCCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----!-----! 300

 S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----!-----! 360

 G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGAG
361 -----!-----!-----!-----!-----!-----! 420

 A G L P Y G A N K D G I I W V A T E G A
GCCGGCTGCGCTACGGCGCCAACAAGGACGGCATCATCTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----!-----! 480

 L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACCAGAAACCCCGCCAACAACGCCGCGCATCGTG
481 -----!-----!-----!-----!-----!-----! 540

 L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----!-----! 600

 G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

 P G S S R G T S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCACCTCTCCTGCGCGGATGGCTGCTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720
 S235F MUTATION
 L A L L L L D R L N Q L E S K M **F** G K G
CTGGCCCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGTTCCGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

 Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCGGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

 R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCTACAACGTGACCCAGGCCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

Figure 47 continued

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCGAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCCAGCGGCACCTGGCTGACCTACACGGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCACCAGAGCCCAAGAGGACAAGAAGAAGGCGGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCGCGCGCC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCAGCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

1: A E P K S C D K T H T C P P C P A P E L
GCCGAGGCCAAATCGTGCGATAAAACGCATACGTGCCCCCTGTCCAGCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCCTGTTCCCCCAAGCCCAAGGACACCCCTGATGATCAGC
1381 -----!-----!-----!-----!-----!-----! 1440

R T P E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGGACGTGAGCCACGAGACCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACACAGCCTGGACCCAGCCAGAGAGGAG
1501 -----!-----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGTACAAGTGCAAGGTGAGCAACAAGGCCCTGCCCGCCCCATCGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCAGACACCCAGGTGTACACCAATACCCCCCTT
1681 -----!-----!-----!-----!-----!-----! 1740

R E Q M S K K K V S L T C L V T N F F S
AGAGAACAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

Figure 47 continued

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      E A I S V E W E S N G Q P E N N Y K T T
      GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

      P P V I D S D G S F F L Y S K L T V D K
      CCCCCCGTGTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

      S R W Q Q G N V F S C S V M H E A L H N
      AGCAGATGGCAGCAGGGCAACGTGTTCTTCTTGCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

      H Y T Q K S L S L S P G K *
      CACTACACCCAGAAGAGCCTGAGCCTGAGCCCCGGCAAGTGATGATCTAAAGGGCGAATT
1981 -----!-----!-----!-----!-----!-----! 2040

      PstI
      CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----! 2064

```

Figure 48. Sequence of pVAXDCSN17; SN17

A: Human IgH Leader + Spike Glycoprotein (AA 319-541) mut B1:351 (SEQ ID NO: 105)

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      BamHI      M D W I W R I L F L V G A A T G
      GGATCCGCCACCATGGACTGGATTGGAGAATCCTCTTCTTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----!-----! 60

      A H S R V Q P T E S I V R F P N I T N L
      GCACACAGCAGAGTGCAGCCCACCGAGAGCATCGTGAGATTCCCCAACATCACCAACCTG
61 -----!-----!-----!-----!-----!-----! 120

      C P F G E V F N A T R F A S V Y A W N R
      TGCCCTTCGGCGAGGTGTTCAACGCCACAGATTGCCAGCGGTACGCCTGGAACAGG
121 -----!-----!-----!-----!-----!-----! 180

      K R I S N C V A D Y S V L Y N S A S F S
      AAGAGAATCAGCAACTGCGTGGCCGACTACAGCGTGCTCTACAACAGCGCCAGCTTCAGC
181 -----!-----!-----!-----!-----!-----! 240

      T F K C Y G V S P T K L N D L C F T N V
      ACCTTCAAGTGCTACGGCGTGAGCCCCACCAAGCTGAACGACCTGTGCTTCACCAACGTG
241 -----!-----!-----!-----!-----!-----! 300

      Y A D S F V I R G D E V R Q I A P G Q T
      TACGCCGACAGCTTCGTGATCAGAGGCGACGAGGTGAGACAGATCGCCCCGGCCAGACC
301 -----!-----!-----!-----!-----!-----! 360

      K417N MUTATION
      G N I A D Y N Y K L P D D F T G C V I A
      GGCAATATCGCGACTACAACACTAAGCTGCCCCGACGACTTCACCGGCTGCGTGATCGCG
361 -----!-----!-----!-----!-----!-----! 420

      W N S N N L D S K V G G N Y N Y L Y R L
      TGGAACAGCAATAACCTGGACAGCAAGGTGGGCGGCAACTACAACCTACCTCTACAGACTG
421 -----!-----!-----!-----!-----!-----! 480

      F R K S N L K P F E R D I S T E I Y Q A
      TTCAGAAAGAGCAACCTGAAGCCCTTCGAGAGAGACATCAGCACCGAGATCTACCAGGCC
481 -----!-----!-----!-----!-----!-----! 540

```

94/121

E484K MUTATION

G S T P C N G V **K** G F N C Y F P L Q S Y
GGCAGCACCCCTGCAACGGCGTGAAGGGCTTCAACTGCTACTTCCCCCTCCAGAGCTAC
541 -----!-----!-----!-----!-----! 600

N501Y MUTATION

G F Q P T **Y** G V G Y Q P Y R V V V L S F
GGCTTCCAGCCCACTACGGCGTGGGCTACCAAGCCCTACAGAGTGGTGGTCTGAGCTTC
601 -----!-----!-----!-----!-----! 660

E L L H A P A T V C G P K K S T N L V K
GAGCTGCTGCACGCCCCCGCCACCGTGTGCGGCCCAAGAAGAGCACCAATCTGGTGAAG
661 -----!-----!-----!-----!-----! 720

N K C V N **E** * **XhoI**
AACAAAGTCCGTGAACTTCTGATG**ACTCGAG**
721 -----!-----!-----! 750

B: Human IgH Leader + Nucleoprotein (AA 2-419) + HuigG1 Hinge-CH2-CH3 iV1 mut B1:351 (murine igG3 23 AA substitutions in bold) (SEQ ID NO:7)

HindIII M D W I W R I L F L V G A A T G
AAGCTTGCCACCATGGACTGGATTGGAGAATCCTCTTCTTGGTGGGAGCTGCCACAGGC
1 -----!-----!-----!-----!-----! 60

A H S S D N G P Q N Q R N A P R I T F G
GCACACAGCAGCGACAACGGCCCCCAGAACCCAGAGAAACGCCCCCAGAATCACCTTCGGC
61 -----!-----!-----!-----!-----! 120

G P S D S T G S N Q N G E R S G A R S K
GGCCCCAGCGACAGCACCGGCAGCAACCAGAACGGCGAGAGAAGCGGCGCCAGAAGCAAG
121 -----!-----!-----!-----!-----! 180

Q R R P Q G L P N N T A S W F T A L T Q
CAGAGAAGACCCAGGGCCTGCCCAACAACACCGCCAGCTGGTTACCGGCCCTGACCCAG
181 -----!-----!-----!-----!-----! 240

H G K E D L K F P R G Q G V P I N T N S
CACGGCAAGGAGGACCTGAAGTTCCCCAGAGGCCAGGGCGTGGCCATCAACACCAACAGC
241 -----!-----!-----!-----!-----! 300

S P D D Q I G Y Y R R A T R R I R G G D
AGCCCCGACGACCAGATCGGCTACTACAGAAGAGCCACCAGAAGAATCAGAGGCGGCGAC
301 -----!-----!-----!-----!-----! 360

G K M K D L S P R W Y F Y Y L G T G P E
GGCAAGATGAAGGACCTGAGCCCCAGATGGTACTTCTACTACCTGGGCACCGGCCCGAG
361 -----!-----!-----!-----!-----! 420

A G L P Y G A N K D G I I W V A T E G A
GCCGGCTTGGCTTACGGCGCCAACAAGGACGGCATCATCTTGGGTGGCCACCGAGGGCGCC
421 -----!-----!-----!-----!-----! 480

L N T P K D H I G T R N P A N N A A I V
CTGAACACCCCCAAGGACCACATCGGCACCAGAAACCCCGCCAACAACGCGCCATCGTG
481 -----!-----!-----!-----!-----! 540

L Q L P Q G T T L P K G F Y A E G S R G
CTCCAGCTGCCCCAGGGCACCACCTGCCCAAGGGCTTCTACGCCGAGGGCAGCAGAGGC
541 -----!-----!-----!-----!-----! 600

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Figure 48 continued

G S Q A S S R S S S R S R N S S R N S T
GGCAGCCAGGCCCTCAAGCCGTTCAGCAGCAGATCCCGCAACAGCTCCCGCAACAGCACC
601 -----!-----!-----!-----!-----!-----! 660

T205I MUTATION

P G S S R G I S P A R M A G N G G D A A
CCTGGAAGCTCAAGGGGCATCTCTCCTGCGCGGATGGCTGGTAACGGCGGGGACGCTGCC
661 -----!-----!-----!-----!-----!-----! 720

L A L I L L D R L N Q L E S K M S G K G
CTGGCCCTGCTGCTGCTGGACAGACTGAACCAGCTGGAGAGCAAGATGAGCGGCAAGGGC
721 -----!-----!-----!-----!-----!-----! 780

Q Q Q Q G Q T V T K K S A A E A S K K P
CAGCAGCAGCAGGGCCAGACTGTGACCAAAAAAGCGCCGCCGAGGCCAGCAAGAAGCCC
781 -----!-----!-----!-----!-----!-----! 840

R Q K R T A T K A Y N V T Q A F G R R G
AGACAGAAGAGAACCGCCACCAAGGCCTACAACGTGACCCAGGCCTTCGGCAGAAGAGGC
841 -----!-----!-----!-----!-----!-----! 900

P E Q T Q G N F G D Q E L I R Q G T D Y
CCCAGCAGACCCAGGGCAACTTCGGCGACCAGGAGCTGATCAGACAGGGCACCGACTAC
901 -----!-----!-----!-----!-----!-----! 960

K H W P Q I A Q F A P S A S A F F G M S
AAGCACTGGCCCCAGATCGCCAGTTTCGCCCCAGCGCCAGCGCCTTCTTCGGCATGAGC
961 -----!-----!-----!-----!-----!-----! 1020

R I G M E V T P S G T W L T Y T G A I K
AGAATCGGCATGGAGGTGACCCCGAGCGGCACCTGGCTGACCTACACCGCGCCATCAAG
1021 -----!-----!-----!-----!-----!-----! 1080

L D D K D P N F K D Q V I L L N K H I D
CTGGACGACAAGGACCCCAACTTCAAGGATCAGGTGATCCTGCTGAACAAGCACATCGAC
1081 -----!-----!-----!-----!-----!-----! 1140

A Y K T F P P T E P K K D K K K K A D E
GCCTACAAGACCTTCCCCCCCACCGAGCCCAAGAGGACAAGAAGAAGAGGCGGACGAG
1141 -----!-----!-----!-----!-----!-----! 1200

T Q A L P Q R Q K K Q Q T V T L L P A A
ACCCAGGCCCTGCCCCAGAGACAGAAGAAGCAGCAGACAGTGACATTGCTGCCCCGCCGC
1201 -----!-----!-----!-----!-----!-----! 1260

D L D D F S K Q L Q Q S M S S A D S T Q
GACCTGGACGACTTCAGCAAGCAGCTCCAGCAGAGCATGAGCAGCGCCGACAGCACCCAG
1261 -----!-----!-----!-----!-----!-----! 1320

A E F K S C D K T H T C P P C P A P E L
GCCGAGCCCAAAATCGTGCATATAAACGCATACGTGCCCCCCTGTCCAGCCCCAGAGTTG
1321 -----!-----!-----!-----!-----!-----! 1380

L G G P S V F L F P P K P K D T L M I S
CTGGGTGGACCGAGCGTGTTCCTGTTCCTGTTCCTGTTCCTGTTCCTGTTCCTGTTCCTGT
1381 -----!-----!-----!-----!-----!-----! 1440

R T F E V T C V V V D V S H E D P E V K
AGAACCCCGAGGTGACCTGCGTGGTGGTGACGTGAGCCACGAGGACCCCGAGGTGAAG
1441 -----!-----!-----!-----!-----!-----! 1500

Figure 48 continued

```
F N W Y V D G V E V H T A W T Q P R E E
TTCAACTGGTACGTGGACGGCGTGGAGGTGCACACAGCCTGGACCCAGCCCAGAGAGGAG
1501 -----!-----!-----!-----!-----! 1560

Q Y N S T Y R V V S V L T V L H Q D W L
CAGTACAACAGCACCTACAGAGTTGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTG
1561 -----!-----!-----!-----!-----!-----! 1620

N G K E Y K C K V S N K A L P A P I E K
AACGGCAAGGAGT'ACAAGT'GCAAGGT'GAGCAACAAGGCCCT'GCCCCGCCCCAT'CGAGAAG
1621 -----!-----!-----!-----!-----!-----! 1680

T I S K P K G R A Q T P Q V Y T I P P P
ACCATCAGCAAGCCCAAGGGCAGAGCCCAGACACCCAGGTGTACACCATACCCCCCCT
1681 -----!-----!-----!-----!-----!-----! 1740

R E Q M S K K K V S L T C L V T N F F S
AGAGAACAATGTCCAAGAAGAAGGTGAGCCTGACCTGCCTGGTGACCAACTTCTTCTCT
1741 -----!-----!-----!-----!-----!-----! 1800

E A I S V E W E S N G Q P E N N Y K T T
GAAGCCATCAGTGTGGAGTGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACC
1801 -----!-----!-----!-----!-----!-----! 1860

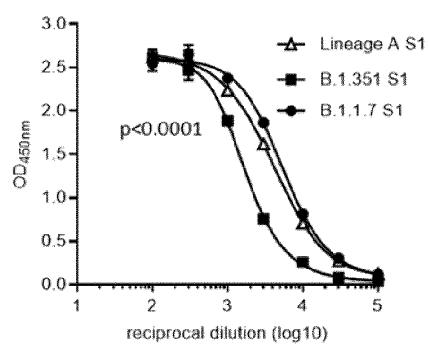
P P V L D S D G S F F L Y S K L T V D K
CCCCCGTGCTGGACAGCGACGGCAGCTTCTTCTCTACAGCAAGCTGACCGTGGACAAG
1861 -----!-----!-----!-----!-----!-----! 1920

S R W Q Q G N V F S C S V M H E A L H N
AGCAGATGGCAGCAGGGCAACGTGTTCTCTTGCAGCGTGATGCACGAGGCCCTGCACAAC
1921 -----!-----!-----!-----!-----!-----! 1980

H Y T Q K S L S L S P G K *
CACTACACCCAGAAGAGCCT'GAGCCT'GAGCCCCGGCAAGT'GATGATCTAAAGGGCGAAT'
1981 -----!-----!-----!-----!-----!-----! 2040

PstI
CGCCCTTAAGGGCTAATTCTGCAG
2041 -----!-----!-----!-----!-----! 2064
```

Figure 49.



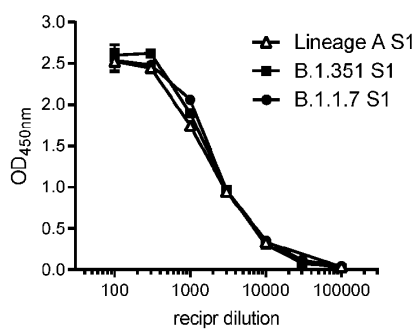
	Lineage A S1	B.1.1.7 S1	B.1.351 S1
EC50	4022	5426	1696
Rsquared	0.9978	0.9966	0.9974

98/121

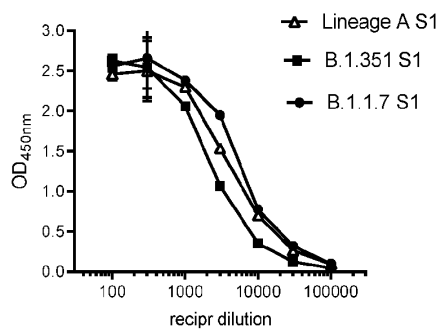
Figure 50.

A.

i. SN17



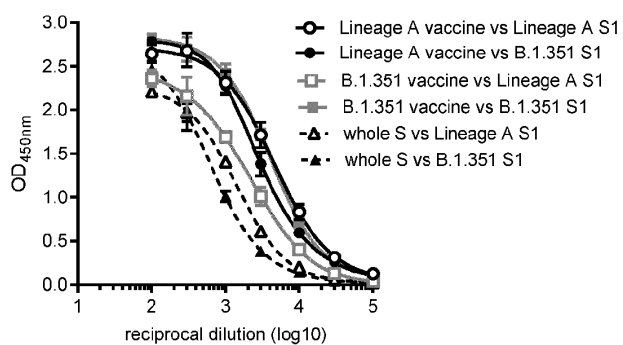
ii. SN16



iii.

	SN17 vaccine			SN16 vaccine		
	Lineage A S1	B.1.1.7 S1	B.1.351 S1	Lineage A S1	B.1.1.7 S1	B.1.351 S1
EC50	1870	2192	1943	4496	5527	2263
R squared	0.9965	0.9978	0.9969	0.9846	0.9840	0.9871

B.

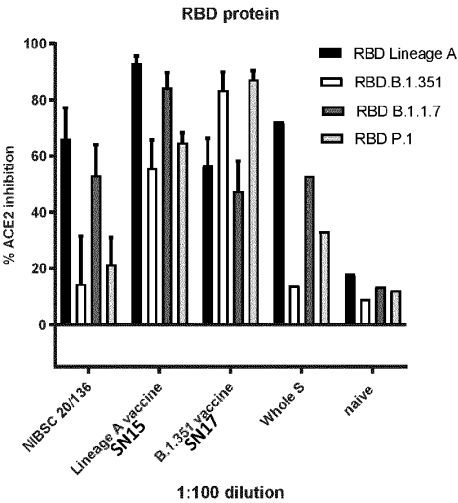


	Lineage A vaccine (SN15)		B.1.351 vaccine (SN17)		Whole S	
	Lineage A S1	B.1.351 S1	Lineage A S1	B.1.351 S1	Lineage A S1	B.1.351 S1
EC50	4664	2949	2086	3931	1389	644
R squared	0.9935	0.9946	0.9913	0.9965	0.9974	0.9947

Figure 50 continued

C.

i.



ii.

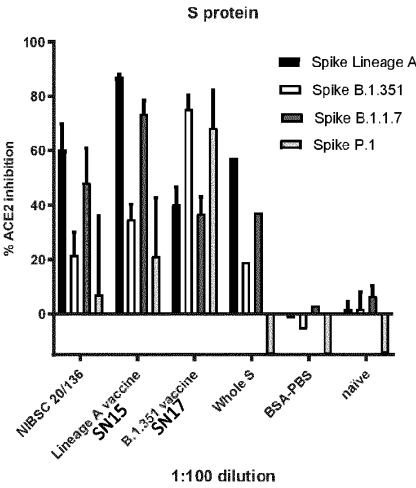
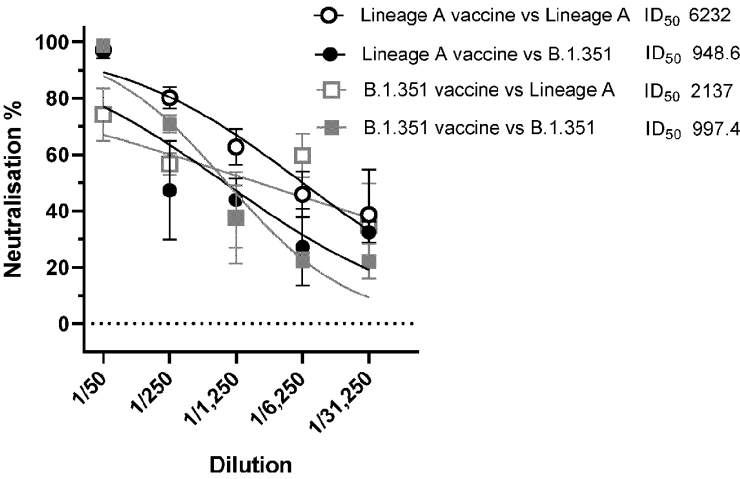


Figure 51.

A.



B.

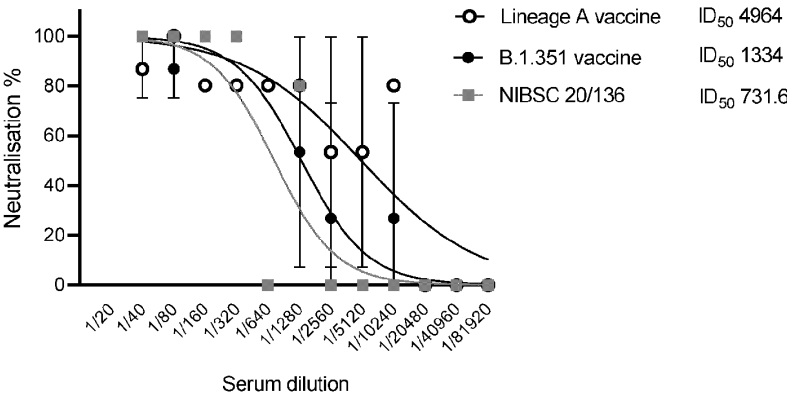


Figure 52.

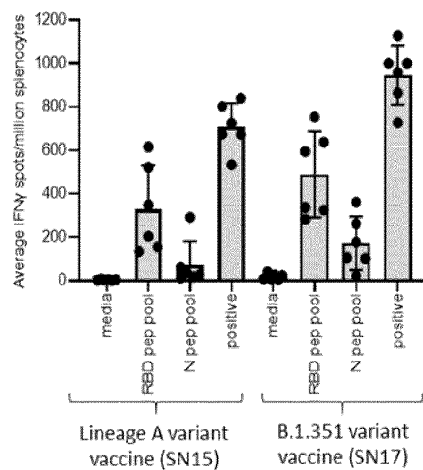
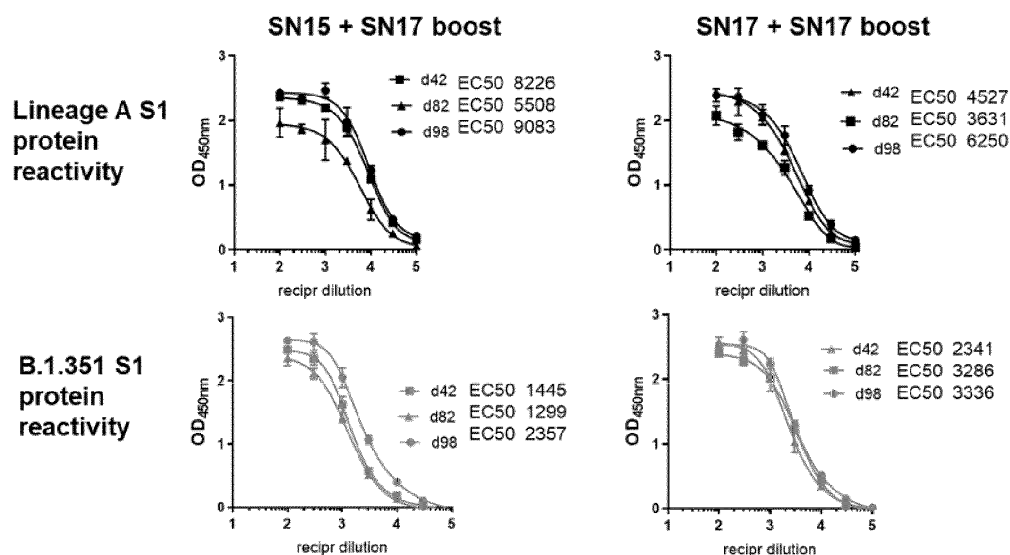


Figure 53.

A.



B.

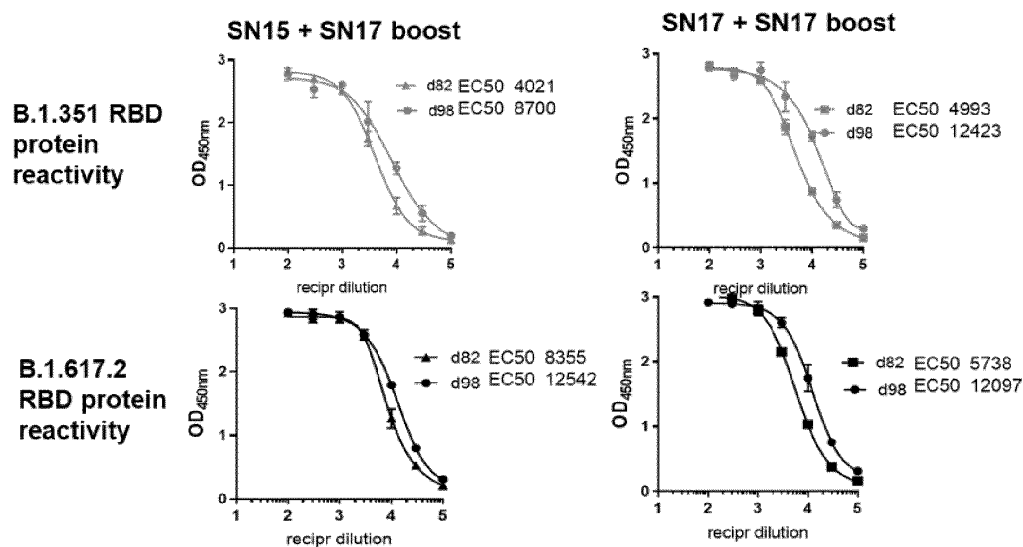


Figure 54

SN15 whole plasmid vector sequence (SEQ ID NO: 23)

```
1      GCTGCTTCGC GATGTACGGG CCAGATATAC GCGTTGACAT TGATTATGA CTAGTTATTA
61     ATAGTAATCA ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
121    ACTTACGGTA AATGGCCCCG CTGGCTGACC GCGCAACGAC CCCCGCCCAT TGACGTCAAT
181    AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC CATTGACGTC AATGGGTGGA
241    GTATTTACGG TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC
301    CCCTATTGAC GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT
361    ATGGGACTTT CTTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT
421    GCGGTTTTGG CAGTACATCA ATGGGCGTGG ATAGCGGTTT GACTCACGGG GATTTCCAAG
481    TCTCCACCCC ATTGACGTCA ATGGGAGTTT GTTTTGGCAC CAAAATCAAC GGGACTTTCC
541    AAAATGTCGT AACAACTCCG CCCCATTGAC GCAAATGGGC GGTAGGCGTG TACGGTGGGA
601    GGTCTATATA AGCAGAGCTC TCTGGCTAAC TAGAGAACCC ACTGCTTACT GGCTTATCGA

                                     BamHI
                                     ~~~~~~
661    AATTAATACG ACTCACTATA GGGAGACCCA AGCTAGCTTG GTACCGAGCT CGGATCCGCC
      M D W I W R I L F L V G A A T G A H S
721    ACCATGGACT GGATTTGGAG AATCCTCTTC CTGGTGGGAG CTGCCACAGG CGCACACAGC
      R V Q P T E S I V R F P N I T N L C P F
781    AGAGTGCAGC CCACCGAGAG CATCGTGAGA TTCCCCAACA TCACCAACCT GTGCCCCCTT
      G E V F N A T R F A S V Y A W N R K R I
841    GGCGAGGTGT TCAACGCCAC CAGATTCGCC AGCGTGTACG CCTGGAACAG GAAGAGAATC
      S N C V A D Y S V L Y N S A S F S T F K
901    AGCAACTGCG TGGCCGACTA CAGCGTGCTC TACAACAGCG CCAGCTTCAG CACCTTCAAG
      C Y G V S P T K L N D L C F T N V Y A D
961    TGCTACGGCG TGAGCCCCAC CAAGCTGAAC GACCTGTGCT TCACCAACGT GTACGCCGAC
      S F V I R G D E V R Q I A P G Q T G K I
1021  AGCTTCGTGA TCAGAGGCGA CGAGGTGAGA CAGATCGCCC CCGGCCAGAC CGGCAAGATC
      A D Y N Y K L P D D F T G C V I A W N S
1081  GCCGACTACA ACTACAAGCT GCCCGACGAC TTCACCGGCT GCGTGATCGC GTGGAACAGC
      N N L D S K V G G N Y N Y L Y R L F R K
1141  AATAACCTGG ACAGCAAGGT GGGCGGCAAC TACAACCTACC TCTACAGACT GTTCAGAAAG
      S N L K P F E R D I S T E I Y Q A G S T
1201  AGCAACCTGA AGCCCTTCGA GAGAGACATC AGCACCGAGA TCTACCAGGC CGGCAGACCC
      P C N G V E G F N C Y F P L Q S Y G F Q
1261  CCCTGCACAG GCGTGGAGGG CTTCAACTGC TACTTCCCCC TCCAGAGTAA GGTCTCCAG
      P T N G V G Y Q P Y R V V V L S F E L L
1321  CCCACCAACG GCGTGGGCTA CCAGCCCTAC AGAGTGGTGG TCCTGAGCTT CGAGCTGCTG
      H A P A T V C G P K K S T N L V K N K C
1381  CACGCCCCCG CCACCGTGTG CGGCCCAAG AAGAGCACCA ATCTGGTGAA GAACAAGTGC

                                     XhoI
                                     ~~~~~~
      V N F * *
1441  GTGAACTTCT GATGACTCGA GCATGCATCT AGAGGGCCCT ATTCTATAGT GTCACCTAAA
1501  TGCTAGAGCT CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
1561  CCCCCTCCCC GTGCCTTCCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCCTAATA
1621  AAATGAGGAA ATTGCATCGC ATTGTCTGAG TAGGTGTCTAT TCTATTCTGG GGGGTGGGGT
1681  GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC AGGCATGCTG GGGATGCGGT
1741  GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGGCTAGCG TTCGATGTAC GGGCCAGATA
1801  TACGCGTTGA CATTGATTAT TGA CTAGTTA TTAATAGTAA TCAATTACGG GGTCAATTAGT
1861  TCATAGCCCA TATATGGAGT TCCGCGTTAC ATAACCTTACG GTAAATGGCC CGCCTGGCTG
1921  ACCGCCCCAAC GACCCCGGCC CATTGACGTC AATAATGACG TATGTTCCCA TAGTAACGCC
1981  AATAGGGACT TTCCATTGAC GTCAATGGGT GGAGTATTTA CGGTAAACTG CCCACTTGGC
2041  AGTACATCAA GTGTATCAIA TGCCAAGTAC GCCCCCTATT GACGTCAATG ACGGTAAATG
2101  GCCGCGCTGG CATTATGCCC AGTACATGAC CTATATGGGAC TTTCTTACTT GGCAGTACAT
2161  CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT TGGCAGTACA TCAATGGGCG
2221  TTGATAGCGG TTTGACTCAC GGGGATTTCC AAGTCTCCAC CCCATTGACG TCAATGGGAG
2281  TTTGTTTTGG CACCAAAATC AACGGGACTT TCCAAAATGT CGTAACAACCT CCGCCCCATT
2341  GACGCAAAATG GGGGTTAGGC GTGTACGGTG GGAGGTCTAT ATAAGCAGAG CTCTCTGGCT
2401  AACTAGAGAA CCCACTGCTT ACTGGCTTAT CGAAATTAAT ACGACTCACT ATAGGGAGAC
```

Figure 54 continued

HindIII
~~~~~

M D W I W R I L

|      |                                                                            |
|------|----------------------------------------------------------------------------|
| 2461 | CCAAGCTGGC TAGCGTTTAA ACTT <b>AAGCTT</b> GCCACCATGG ACTGGATTTG GAGAATCCTC  |
|      | F L V G A A T G A H S S D N G P Q N Q R                                    |
| 2521 | TTCTGGTGG GAGCTGCCAC AGGCGCACAC AGCAGCGACA ACGGCCCCCA GAACCAGAGA           |
|      | N A P R I T F G G P S D S T G S N Q N G                                    |
| 2581 | AACGCCCCCA GAATCACCTT CGGCGGCCCC AGCGACAGCA CCGGCAGCAA CCAGAACGGC          |
|      | E R S G A R S K Q R R P Q G L P N N T A                                    |
| 2641 | GAGAGAAGCG GCGCCAGAAG CAAGCAGAGA AGACCCAGG GCCTGCCCCA CAACACCGCC           |
|      | S W F T A L T Q H G K E D L K F P R G Q                                    |
| 2701 | AGCTGGTTCA CCGCCCTGAC CCAGCACGGC AAGGAGGACC TGAAGTTCCC CAGAGGCCAG          |
|      | G V P I N T N S S P D D Q I G Y Y R R A                                    |
| 2761 | GGCGTGCCCA TCAACACCAA CAGCAGCCCC GACGACCAGA TCGGCTACTA CAGAAGAGCC          |
|      | T R R I R G G D G K M K D L S P R W Y F                                    |
| 2821 | ACCAGAAGAA TCAGAGGCGG CGACGGCAAG ATGAAGGACC TGAGCCCCAG ATGGTACTTC          |
|      | Y Y L G T G P E A G L P Y G A N K D G I                                    |
| 2881 | TACTACCTGG GCACCGGCCC CGAGGCCGGC CTGCCCTACG GCGCCAACAA GGACGGCATC          |
|      | I W V A T E G A L N T P K D H I G T R N                                    |
| 2941 | ATCTGGGTGG CCACCGAGGG CGCCCTGAAC ACCCCCAAGG ACCACATCGG CACCAGAAAC          |
|      | P A N N A A I V L Q L P Q G T T L P K G                                    |
| 3001 | CCCGCCAACA ACGCCGCCAT CGTGCTCCAG CTGCCCCAGG GCACCACCTT GCCCAAGGGC          |
|      | F Y A E G S R G G S Q A S S R S S S R S                                    |
| 3061 | TTCTACGCCG AGGGCAGCAG AGGCGGCAGC CAGGCCTCAA GCCGTTCCAG SAGCAGATCC          |
|      | R N S S R N S T P G S S R G T S P A R M                                    |
| 3121 | CGCAACAGCT CCCGCAACAG CACCCCTGGA AGTCAAGGG GCACCTCTCC TGC GCGGATG          |
|      | A G N G G D A A L A L L L L D R L N Q L                                    |
| 3181 | GCTGGTAACG GCGGGGACGC TGCCTTGCCC CTGCTGCTGC TGGACAGACT GAACCAAGTG          |
|      | E S K M S G K G Q Q Q Q G Q T V T K K S                                    |
| 3241 | GAGAGCAAGA TGAGCGGCAA GGGCCAGCAG CAGCAGGGCC AGACTGTGAC CAAAAAAGC           |
|      | A A E A S K K P R Q K R T A T K A Y N V                                    |
| 3301 | GCCGCCGAGG CCAGCAAGAA GCCCAGACAG AAGAGAACCG CCACCAAGGC CTACAACGTG          |
|      | T Q A F G R R G P E Q T Q G N F G D Q E                                    |
| 3361 | ACCCAGGCCT TCGGCAGAAG AGGCCCCGAG CAGACCCAGG GCAACTTCGG CGACCAGGAG          |
|      | L I R Q G T D Y K H W P Q I A Q F A P S                                    |
| 3421 | CTGATCAGAC AGGGCACCGA CTACAAGCAC TGGCCCCAGA TCGCCCAAGT CGCCCCAGS           |
|      | A S A F F G M S R I G M E V T P S G T W                                    |
| 3481 | GCCAGCGCCT TCTTCGGCAT GAGCAGAATC GGCATGGAGG TGACCCCGAG CGGCACCTGG          |
|      | L T Y T G A I K L D D K D P N F K D Q V                                    |
| 3541 | CTGACCTACA CCGGCGCCAT CAAGCTGGAC GACAAGGACC CCAACTTCAA GGATCAGTGTG         |
|      | I L L N K H I D A Y K T F P P T E P K K                                    |
| 3601 | ATCTGCTGA ACAAGCACAT CGACGCCTAC AAGACCTTCC CCCCACCGA GCCCAAGAAG            |
|      | D K K K K A D E T Q A L P Q R Q K K Q Q                                    |
| 3661 | GACAAGAAGA AGAAGGCCGA CGAGACCCAG GCCCTGCCCC AGAGACAGAA GAAGCAGCAG          |
|      | T V T L L P A A D L D D F S K Q L Q Q S                                    |
| 3721 | ACAGTGACAT TGCTGCCCGC CGCCGACCTG GACGACTTCA GCAAGCAGCT CCAGCAGAGC          |
|      | M S S A D S T Q A E P K S C D K T H T C                                    |
| 3781 | ATGAGCAGCG CCGACAGCAC CCAGGCCGAG CCCAAATCGT GCGATAAAAC GCATACGTGC          |
|      | P P C P A P E L L G G P S V F L F P P K                                    |
| 3841 | CCCCCTGTG CAGCCCCAGA GTTGCTGGGT GGACCGAGCG TGTTCCTGTT CCCCCCAAG            |
|      | P K D T L M I S R T P E V T C V V V D V                                    |
| 3901 | CCCAAGGACA CCTGATGAT CAGCAGAACC CCCGAGGTGA CCTGCGTGTT GGTGGACGTG           |
|      | S H E D P E V K F N W Y V D G V E V H T                                    |
| 3961 | AGCCACGAGG ACCCCGAGG' GAAGTTCAAC TGGTACGTGG ACGGCGTGGG GGTGCACACA          |
|      | A <b>W</b> T <b>Q</b> P R E E Q Y N S T Y R V V S V L                      |
| 4021 | GCCTGGACCC AGCCCAGAGA GGAGCAGTAC AACAGCACCT ACAGAGTTGT GTCCGTGCTG          |
|      | T V L H Q D W L N G K E Y K C K V S N K                                    |
| 4081 | ACCGTGCTGC ACCAGGACTG GCTGAACGGC AAGGAGTACA AGTGCAAGGT GAGCAACAAG          |
|      | A L P A P I E K T I S K <b>P</b> K G <b>R</b> <b>A</b> <b>Q</b> <b>T</b> P |
| 4141 | GCCCTGCCCG CCCCATCGA GAAGACCATC AGCAAGCCCA AGGGCAGAGC CCAGACACCC           |

Figure 54 continued

```
Q V Y T I P P P R E Q M S K K K V S L T
4201 CAGGTGTACA CCATACCCC CCCTAGAGAA CAAATGTCCA AGAAGAAGGT GAGCCTGACC
      C L V T N F F S E A I S V E W E S N G Q
4261 TGCCTGGTGA CCAACTTCTT CTCTGAAGCC ATCAGTGTGG AGTGGGAGAG CAACGGCCAG
      P E N N Y K T T P P V L D S D G S F F L
4321 CCCGAGAACA ACTACAAGAC CACCCCCCCC GTGCTGGACA GCGACGGCAG CTCTCTCCTC
      Y S K L T V D K S R W Q Q G N V F S C S
4381 TACAGCAAGC TGACCGTGGG CAAGAGCAGA TGGCAGCAGG GCAACGTGTT CTCTTGACGC
      V M H E A L H N H Y T Q K S L S L S P G
4441 GTGATGCACG AGGCCCTGCA CAACCACTAC ACCCAGAAGA GCCTGAGCCT GAGCCCCGGC

      EcoRI                               PstI
      ~~~~~~                               ~~~~~~

K * *
4501 AAGTGATGAT CTAAAGGGCG AATTGCGCCT TAAGGGCTAA TTCTGCAGAT TCGAGCATGC
4561 ATCTAGAGGG CCCGTTTAAA CCGCTGATC AGCCTCGACT GTGCCTTCTA GTTGCCAGCC
4621 ATCTGTGTGT TGGCCCTCCC CCGTGCCTTC CTTGACCCTG GAAGGTGCCA CTCCCCTGT
4681 CCTTTCCTAA TAAATGAGG AAATTGCATC GCATTGTCTG AGTAGGTGTC ATTCTATTCT
4741 GGGGGGTGGG GTGGGGCAGG ACAGCAAGGG GGAGGATTTG GAAGACAATA CGAGGCATGC
4801 TGGGGATGCG GTGGGCTCTA TGGCTTCTAC TGGGCGGTTT TATGGACAGC AAGCGAACC
4861 GAATTGCCAG CTGGGGCGCC CTCTGGTAAG GTTGGGAAGC CCTGCAAAGT AAACCTGATG
4921 GCTTTCCTGC CGCAAGGAT CTGATGGCGC AGGGGATCAA GCTCTGATCA AGAGACAGGA
4981 TGAGGATCGT TTCGCATGAT TGAACAAGAT GGATTGCACG CAGGTTCTCC GGCCGCTTGG
5041 GTGGAGAGGC TATTCGGCTA TGAATGGGCA CAACAGACAA TCGGCTGCTC TGATGCCGCC
5101 GTGTTCCGGC TGTGAGCGCA GGGGCGCCCG GTTCTTTTTC TCAAGACCGA CCTGTCCGGT
5161 GCCCTGAATG AACTGCAAGA CGAGGCAGCG CGGCTATCGT GGCTGGCCAC GACGGGCGTT
5221 CCTTGCGCAG CTGTGCTCGA CGTTGTCACT GAAGCGGGAA GGGACTGGCT GCTATTGGGC
5281 GAAGTGCCGG GGCAGGATCT CCGTCACTC CACCTTGCTC CTGCCGAGAA AGTATCCATC
5341 ATGGCTGATG CAATGCGGCG GCTGCATACG CTTGATCCGG CTACCTGCCA ATTCGACCAC
5401 CAAGCGAAAC ATCGCATCGA GCGAGCACGT ACTCGGATGG AAGCCGGTCT TGTGATCAG
5461 GATGATCTGG ACGAAGAGCA TCAGGGGCTC GCGCCAGCCG AACTGTTGCG CAGGCTCAAG
5521 GCGAGCATGC CCGACGGCGA GGATCTCGTC GTGACCCATG GCGATGCTG CTTGCCGAAT
5581 ATCATGGTGG AAAATGGCCG CTTTCTGGA TTCATCGACT GTGGCCGGCT GGGTGTGGCG
5641 GACCGCTATC AGGACATAGC GTTGGCTACC CGTGATAATT CTGAAGAGCT TGGCGGCGAA
5701 TGGGCTGACC GCTTCCTCGT GCTTTACGGT ATCGCCGCTC CCGATTGCGA GCGCATCGCC
5761 TTCTATCGCC TTCTTGACGA GTTCTTCTGA ATTATTAACG CTTACAATTT CCTGATGCGG
5821 TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TCAGGTGGCA CTTTTCGGGG
5881 AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT
5941 CATGAGACAA TAACCTGAT AAATGCTTCA ATAATAGCAC GTGCTAAAAC TTCATTTTTA
6001 ATTTAAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG
6061 TGAGTTTTTC TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA
6121 TCCTTTTTTT CTGCGCTTAA TCTGCTGCTT GCAAACAAAA AAACCACCGC TACCAGCGGT
6181 GGTTTGTGTT CCGGATCAAG AGTACCAAC TCTTTTTTCC AAGGTAACGT GCTTCAGCAG
6241 AGCGCAGATA CCAAACTATG TTCTTCTAGT GTAGCCGTAG TTAGGCCACC ACTTCAAGAA
6301 CTCTGTAGCA CCGCTACAT ACCTCGCTCT GCTAATCCTG TTACCACTGG CTGCTGCCAG
6361 TGGCGATAAG TCGTGTCTTA CCGGTTTGA CTAAGACGA TAGTTACCGG ATAAGGCGCA
6421 GCGTCCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA CGACCTACAC
6481 CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA
6541 GCGGACAGG TATCCGGTAA CCGGCAGGGT CGGAACAGGA GAGCGCACGA GGGAGCTTCC
6601 AGGGGGAAC GCCTGGTATC TTTATAGTCC TGTGCGGTTT CGCCACCTCT GACTTGAGCG
6661 TCGATTTTTG TGATGCTCGT CAGGGGGGCG GAGCCTATGG AAAACGCCA GCAACGCGCG
6721 CTTTTCACG TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTTCTT
```

Figure 55

SN17 whole plasmid vector sequence (SEQ ID NO: 24)

```
1 GCTGCTTCGC GATGTACGGG CCAGATATAC GCGTTGACAT TGATTATGA CTAGTTATTA
61 ATAGTAATCA ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
121 ACTTACGGTA AATGGCCCGC CTGGCTGACC GCCCAACGAC CCCCGCCCAT TGACGTCAAT
181 AATGACGTAT GTTCCCATAG TAACGCCAA AGGGACTTTC CATTGACGTC AATGGGTGGA
241 GTATTTACGG TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC
301 CCTATTGAC GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT
361 ATGGGACTTT CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT
421 GCGGTTTTGG CAGTACATCA ATGGGCGTGG ATAGCGGTTT GACTCACGGG GATTTCCAAG
481 TCTCCACCCC ATTGACGTCA ATGGGAGTTT GTTTTGGCAC CAAAATCAAC GGGACTTTC
541 AAAATGTCGT AACAACCTCC CCCCATTGAC GCAAAATGGG GGTAGGCGTG TACGGTGGGA
601 GGCTATATA AGCAGAGCTC TCTGGCTAAC TAGAGAACCC ACTGCTTACT GGCTTATCGA

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                                     ~~~~~~
661    AATTAATACG  ACTCACTATA  GGGAGACCCA  AGCTAGCTTG  GTACCGAGCT  CCGATCCGCC
      M D W I W R I L F L V G A A T G A H S
721    ACCATGGACT  GGATTTGGAG  AATCCTCTTC  CTGGTGGGAG  CTGCCACAGG  CGCACACAGC
      R V Q P T E S I V R F P N I T N L C P F
781    AGAGTGCAGC  CCACCGAGAG  CATCGTGAGA  TTCCCAACA  TCACCAACCT  GTGCCCCTTC
      G E V F N A T R F A S V Y A W N R K R I
841    GGCGAGGTGT  TCAACGCCAC  CAGATTCGCC  AGCGTGACG  CCTGGAACAG  GAAGAGAATC
      S N C V A D Y S V L Y N S A S F S T F K
901    AGCAACTGCG  TGGCCGACTA  CAGCGTGCTC  TACAACAGCG  CCAGCTTCAG  CACCTTCAAG
      C Y G V S P T K L N D L C F T N V Y A D
961    TGCTACGGCG  TGAGCCCCAC  CAAGCTGAAC  GACCTGTGCT  TCACCAACGT  GTACGCCGAC

                                     K417N
      S F V I R G D E V R Q I A P G Q T G N I
1021  AGCTTCGTGA  TCAGAGGCGA  CGAGGTGAGA  CAGATCGCCC  CCGGCCAGAC  CGGCAATATC
      A D Y N Y K L P D D F T G C V I A W N S
1081  GCGGACTACA  ACTACAAGCT  GCGGACGAC  TTCACCGGCT  GCGTGATCGC  GTGGAACAGC
      N N L D S K V G G N Y N Y L Y R L F R K
1141  AATAACCTGG  ACAGCAAGGT  GGGCGGCAAC  TACAACCTACC  TCTACAGACT  GTTCAGAAAG
      S N L K P F E R D I S T E I Y Q A G S T
1201  AGCAACCTGA  AGCCCTTCGA  GAGAGACATC  AGCACCAGAG  TCTACCAGGC  CGGCAGCACC

                                     E484K
      P C N G V K G F N C Y F P L Q S Y G F Q
1261  CCTTGCACAC  GCGTGAAGGG  CTTCAACTGC  TACTTCCCC  TCCAGAGCTA  CGGCTTCCAG

                                     N501Y
      P T Y G V G Y Q P Y R V V V L S F E L L
1321  CCCACCTACG  GCGTGGGCTA  CCAGCCCTAC  AGAGTGGTGG  TCCTGAGCTT  CGAGCTGCTG
      H A P A T V C G P K K S T N L V K N K C
1381  CACGCCCCCG  CCACCGTGTG  CGGCCCCAAG  AAGAGCACCA  ATCTGGTGAA  GAACAAGTGC

                                     XhoI
                                     ~~~~~~
 V N F * *
1441 GTGAACTTCT GATGACTCGA GCATGCATCT AGAGGGCCCT ATTCTATAGT GTCACCTAAA
1501 TGCTAGAGCT CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
1561 CCCCTCCCC GTGCCTTCCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCCTAATA
1621 AAATGAGGAA ATTGCATCGA ATTGTCTGAG TAGGTGTCAT TCTATTCTGG GGGGTGGGGT
1681 GGGGACAGG AGCAAGGGGG AGGATTGGGA AGACAATAGC AGGCATGCTG GGGATGCGGT
1741 GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGGCTAGCG TTCGATGTAC GGGCCAGATA
1801 TACGCGTTGA CATTGATTAT TGAAGTAGTA TTAATAGTAA TCAATTACGG GGTCTATTAGT
1861 TCATAGCCCA TATATGGAGT TCCGCGTTAC ATAACTTACG GTAAATGGCC CGCCTGGCTG
1921 ACCGCCAAC GACCCCGGCC CATTGACGTC AATAATGACG TATGTTCCCA TAGTAACGCC
1981 AATAGGACT TTCCATTGAC GTCAATGGGT GGAGTATTTA CGGTAACTG CCCACTTGGC
2041 AGTACATCAA GTGTATCATA TGCCAAGTAC GCCCCCTATT GACGTCAATG ACGGTAAATG
2101 CCGCGCCTGG CATTATGCCC AGTACATGAC CTTATGGGAC TTTCCTACTT GGCAGTACAT
2161 CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGGTTT TGGCAGTACA TCAATGGCGC
2221 TGGATAGCGG TTTGACTCAC GGGGATTTC AAGTCTCCAC CCCATTGACG TCAATGGGAG
2281 TTTGTTTTGG CACCAAAATC AACGGGACTT TCCAAAATGT CGTAACAACT CCGCCCCATT
2341 GACGCAAAAT GGGCGTAGGC GTGTACGGTG GGAGGTCTAT ATAAGCAGAG CTCTCTGGCT
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Figure 55 continued

2401 AACTAGAGAA CCCACTGCTT ACTGGCTTAT CGAAATTAAT ACGACTCACT ATAGGGAGAC  
HindIII  
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2461 CCAAGCTGGC TAGCGTTTAA ACTTAAGCTT GCCACCATGG ACTGGATTGT GAGAATCCTC  
F L V G A A T G A H S S D N G P Q N Q R  
2521 TTCCTGGTGG GAGCTGCCAC AGGCGCACAC AGCAGCGACA ACGGCCCCCA GAACCAAGAGA  
N A P R I T F G G P S D S T G S N Q N G  
2581 AACGCCCCCA GAATCACCTT CGGCGGCCCC AGCGACAGCA CCGGCAGCAA CCAGAACGGC  
E R S G A R S K Q R R P Q G L P N N T A  
2641 GAGAGAAGCG GCGCCAGAAG CAAGCAGAGA AGACCCAGG GCTGCCCAA CAACACCGCC  
S W F T A L T Q H G K E D L K F P R G Q  
2701 AGCTGGTTCA CCGCCCTGAC CCAGCACGGC AAGGAGGACC TGAAGTTCCC CAGAGGCCAG  
G V P I N T N S S P D D Q I G Y Y R R A  
2761 GCGGTGCCCA TCAACACCAA CAGCAGCCCC GAGCACCAGA TCGGCTACTA CAGAAGAGCC  
T R R I R G G D G K M K D L S P R W Y F  
2821 ACCAGAAGAA TCAGAGGCGG CGACGGCAAG ATGAAGGACC TGAGCCCCAG ATGGTACTTC  
Y Y L G T G P E A G L P Y G A N K D G I  
2881 TACTACCTGG GCACCGGCCC CGAGGCGGGC CTGCCCTACG GCGCCAACAA GGACGGCATC  
I W V A T E G A L N T P K D H I G T R N  
2941 ATCTGGGTGG CCACCGAGGG CGCCCTGAAC ACCCCCAAGG ACCACATCGG CACCAGAAAC  
P A N N A A I V L Q L P Q G T T L P K G  
3001 CCCGCCAACA ACGCCGCCAT CGTGCTCCAG CTGCCCCAGG GCACCACCCT GCCCAAGGGC  
F Y A E G S R G G S Q A S S R S S S R S  
3061 TTCTACGCCG AGGGCAGCAG AGGCGGCAGC CAGGCTCAA GCCGTTCAG CAGCAGATCC  
T2051  
R N S S R N S T P G S S R G I S P A R M  
3121 CGCAACAGCT CCCGCAACAG CACCCCTGGA AGCTCAAGGG GCATCTCTCC TGC CGGATG  
A G N G G D A A L A L L L L D R L N Q L  
3181 GCTGGTAACG GCGGGGACGC TGCCCTGGCC CTGCTGCTGC TGGACAGACT GAACCACTG  
E S K M S G K G Q Q Q Q G Q T V T K K S  
3241 GAGACAAGA TGAGCGGCAA GGGCCAGCAG CAGCAGGGCC AGACTGTGAC CAAAAAAGC  
A A E A S K K P R Q K R T A T K A Y N V  
3301 GCCGCCGAGG CCAGCAAGAA GCCCAGACAG AAGAGAACCG CCACCAAGGC TACAACGTG  
T Q A F G R R G P E Q T Q G N F G D Q E  
3361 ACCAGGCCCT TCGGCAGAAG AGGCCCCGAG CAGACCCAGG GCAACTTCGG CGACCAAGAG  
L I R Q G T D Y K H W P Q I A Q F A P S  
3421 CTGATCAGAC AGGGCACCGA CTACAAGCAC TGGCCCCAGA TCGCCCACTT CGCCCCAGC  
A S A F F G M S R I G M E V T P S G T W  
3481 GCCAGCGCCT TCTTCGGCAT GAGCAGAATC GGATGGAGG TGACCCCGAG CAGCACTGG  
L T Y T G A I K L D D K D P N F K D Q V  
3541 CTGACCTACA CCGCGCCCAT CAAGCTGGAC GACAAGGACC CCAACTTCAA GGATCAGGTG  
I L L N K H I D A Y K T F P P T E P K K  
3601 ATCCTGCTGA ACAAGCACAT CGACGCCTAC AAGACCTTCC CCCCCACGA GCCCAAGAG  
D K K K K A D E T Q A L P Q R Q K K Q Q  
3661 GACAAGAAGA AGAAGGCCGA CGAGACCCAG GCCCTGCCCC AGAGACAGAA GAAGCAGCAG  
T V T L L P A A D L D D F S K Q L Q Q S  
3721 ACAGTGACAT TGCTGCCCCG CGCCGACCTG GACGACTTCA GCAAGCAGCT CCAGCAGAGC  
M S S A D S T Q A E P K S C D K T H T C  
3781 ATGAGCAGCG CCGACAGCAC CCAGGCCGAG CCCAAATCGT GCGATAAAAC GCATACGTGC  
P P C P A P E L L G G P S V F L F P P K  
3841 CCCCCGTGTC CAGCCCCAGA GTTGCTGGGT GGACCGAGCG TGTTCTGTG CCCCCCAAG  
P K D T L M I S R T P E V T C V V V D V  
3901 CCCAAGGACA CCCTGATGAT CAGCAGAACC CCCGAGGTGA CTTGCGTGGT GGTGGACGTG  
S H E D P E V K F N W Y V D G V E V H T  
3961 AGCCACGAGG ACCCCGAGGT GAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCACACA  
A W T Q P R E E Q Y N S T Y R V S V L  
4021 GCCTGGACCC AGCCAGAGA GGAGCAGTAC AACAGCACCT ACAGAGTTGT GTCCGTGCTG  
T V L H Q D W L N G K E Y K C K V S N K  
4081 ACCGTGCTGC ACCAGGACTG GCTGAACGGC AAGGAGTACA AGTGCAAGGT GAGCAACAAG

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Figure 55 continued

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 A L P A P I E K T I S K P K G R A Q T P
4141 GCCCTGCCCG CCCCATCGA GAAGACCATC AGCAAGCCCA AGGGCAGAGC CCAGACACCC
 Q V Y T I P P P R E Q M S K K K V S L T
4201 CAGGTGTACA CCATACCCCC CCCTAGAGAA CAAATGTCCA AGAAGAAGGT GAGCCTGACC
 C L V T N F F S E A I S V E W E S N G Q
4261 TGCCTGGTGA CCAACTTCTT CTCTGAAGCC ATCAGTGTGG AGTGGGAGAG CAACGGCCAG
 P E N N Y K T T P P P V L D S D G S F F L
4321 CCCGAGAACA ACTACAAGAC CACCCCCCCC GTGCTGGACA GCGACGGCAG CTTCTTCTTC
 Y S K L T V D K S R W Q Q G N V F S C S
4381 TACAGCAAGC TGACCGTGGG CAAGAGCAGA TGGCAGCAGG GCAACGTGTT CTCTTGACGC
 V M H E A L H N H Y T Q K S L S L S P G
4441 GTGATGCACG AGGCCCTGCA CAACCACTAC ACCCAGAAGA GCCTGAGCCT GAGCCCCGGC

 EcoRI PstI
      ~~~~~                               ~~~~~

      K * *
4501 AAGTGATGAT CTAAAGGGCG AATTCGCCCT TAAGGGCTAA TTCTGCAGAT TCGAGCATGC
4561 ATCTAGAGGG CCGGTTTAA CCGCTGATC AGCCTCGACT GTGCCTTCTA GTTGCCAGCC
4621 ATCTGTTGTT TGGCCCTCCC CCGTGCCCTC CTGACCCCTG GAAGGTGCCA CTCCCCTGT
4681 CCTTTCCTAA TAAATGAGG AAATTGCATC GCATTGTCTG AGTAGGTGTC ATCTAATCT
4741 GGGGGGTGGG GTGGGGCAGG ACAGCAAGGG GGAGGATTGG GAAGACAATA GCAGGCATGC
4801 TGGGGATGCG GTGGGCTCTA TGGCTTCTAC TGGGCGGTTT TATGGACAGC AAGCGAACCG
4861 GAATTGCCAG CTGGGGCGCC CTCTGGTAAG GTTGGGAAGC CTTGCAAAGT AAAGTGGATG
4921 GCTTCTTTCG CGCCAAGGAT CTGATGGCGC AGGGGATCAA GCTCTGATCA AGAGACAGGA
4981 TGAGGATCGT TTCGCATGAT TGAACAAGAT GGATTGCACG CAGGTTCTCC GGCCGCTTGG
5041 GTGGAGAGGC TATTCGGCTA TGAATGGGCA CAACAGACAA TCGGCTGCTC TGATGCCGCC
5101 GTGTTCCGGC TGTGAGCGCA GGGGCGCCCG GTTCTTTTTC TCAAGACCGA CCTGTCCGGT
5161 GCCCTGAATG AACTGCAAGA CGAGGCAGCG CGGCTATCGT GGCTGGCCAC GACGGGCGTT
5221 CCTTGCGCAG CTGTGCTCGA CGTTGTCACT GAAGCGGGAA GGGACTGGCT GCTATTGGGC
5281 GAAGTGCCGG GGCAGGATCT CTTGTCACT CACCTTGCTC CTGCCGAGAA AGTATCCATC
5341 ATGCTGATG CAATGCGGCG GCTGCATACG CTGATCCGG CTACCTGCCC ATTCGACCAC
5401 CAAGCGAAAC ATCGCATCGA GCGAGCACGT ACTCGGATGG AAGCCGGTCT TGTGATCAG
5461 GATGATCTGG ACGAAGAGCA TCAGGGGCTC GCGCCAGCCG AACTGTTTCG CAGGCTCAAG
5521 GCGAGCATGC CCGACGGCGA GGATCTCGTC GTGACCCATG GCGATGCCTG CTTGCCGAAT
5581 ATCATGGTGG AAAATGGCCG CTTTCTGGA TTCTATCGACT GTGGCCGGCT GGGTGTGGCG
5641 GACCGCTATC AGGACATAGC GTTGGCTACC CGTGATATTG CTGAAGAGCT TGGCGGCGAA
5701 TGGGCTGACC GCTTCTCTGT GCTTACGGT ATCGCCGCTC CCGATTGCA GCGCATCGCC
5761 TTCTATCGCC TTCTTGACGA GTTCTTCTGA ATTATTAACG CTTACAATTT CCTGATGCGG
5821 TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TCAGGTGGCA CTTTTCGGGG
5881 AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT
5941 CATGAGACAA TAACCTGAT AAATGCTTCA ATAATAGCAC GTGCTAAAAC TTCATTTTTA
6001 ATTTAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG
6061 TGAGTTTTTC TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA
6121 TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACCACCGC TACCAGCGGT
6181 GGTGTGTTTG CCGGATCAAG AGCTACCAAC TCTTTTTTCG AAGGTAAC TGCTTACGAG
6241 AGCGCAGATA CCAAATACTG TTCTTCTAGT GTAGCCGTAG TTAGGCCACC ACTTCAAGAA
6301 CTCTGTAGCA CCGCTACAT ACCTCGCTCT GCTAATCCTG TTACCACTGG CTGCTGCCAG
6361 TGGCGATAAG TCGTGTCTTA CCGGGTTTGA CTCAAGACGA TAGTTACCGG ATAAGGCGCA
6421 GCGGTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA CGACCTACAC
6481 CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA
6541 GCGGACAGG TATCCGGTAA GCGGAGGGT CGGAACAGGA GAGCGCACGA GGGAGCTTCC
6601 AGGGGGAAC GCCTGGTATC TTTATAGTCC GTTCGGGTTT CGCCACCTCT GACTTGAGCG
6661 TCGATTTTTG TGATGCTCGT CAGGGGGGCG GAGCCTATGG AAAACGCCA GCAACGCGC
6721 CTTTTCACG TTTCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTTCTT

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Figure 56

SN17 whole doggybone (dbDNA) vector sequence (SEQ ID NO: 25)

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1   GCGTATAATG GACTATTGTG TGCTGATATG TACACCTGAG GACACAGGTA CAGGACTCAG
61  CTTAAGGCTA CATCTTAGCT TACGTCATA GAGGGTCCAC GTTTAGTTTT TAAGATCCAT
121 TGATCTCCTA AACGCTGCAA GATTCGCAAC CTGGAATACT TAGCGCTAGG TCCTAGTGAA
181 GCGGGACTTT TTTTCTAAAG TCGTTGAGAG GAGGAGTCGT CAGACCAGAT AGCTTTGATG
241 TCCTGATCGG AAGGATCGTT GCGCCCGATG TACGGGCCAG ATATACGCGT TGACATTGAT
301 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC CCATATATGG
361 AGTTCGCGCT TACATAACTT ACGGTAAATG GCGCGCTGG CTGACCGCCC AACGACCCCC
421 GCGCATTTGAC GTCAATAATG ACGTATGTTT CCATAGTAAC GCCAATAGGG ACTTTCCATT
481 GACGTCAATG GGTGGAGTAT TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC
541 ATATGCCAAG TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCCGC TGGCATTTATG
601 CCCAGTACAT GACCTTATGG GACTTTCCCTA CTTGGCAGTA CATCTACGTA TTAGTCATCG
661 CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG GCGTGGATAG CGGTTTGACT
721 CACGGGGATT TCCAAGTCTC CACCCCATG ACGTCAATGG GAGTTTGTIT TGGCACCAAA
781 ATCAACGGGA CTTTCCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGTA
841 GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCTCTG GCTAAGTAGA GAACCCACTG
901 CTTACTGGCT TATCGAAATT AATACGACTC ACTATAGGGA GACCCAAGCT AGCTTGGTAC

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      ~~~~~~
 M D W I W R I L F L V G A A

961 CGAGCTCGGA TCCGCCACCA TGGACTGGAT TTGGAGAATC CTCTTCCTGG TGGGAGCTGC
 · T G A H S R V Q P T E S I V R F P N I T

1021 CACAGGCGCA CACAGCAGAG TGAGGCCAC CGAGAGCATC GTGAGATTCC CCAACATCAC
 · N L C P F G E V F N A T R F A S V Y A W

1081 CAACCTGTGC CCCTTCGGCG AGGTGTTCAA CGCCACCAGA TTCGCCAGCG TGTACGCTG
 · N R K R I S N C V A D Y S V L Y N S A S

1141 GAACAGGAAG AGAATCAGCA ACTGCGTGGC CGACTACAGC GTGCTCTACA ACAGCGCCAG
 · F S T F K C Y G V S P T K L N D L C F T

1201 CTTCAGCACC TTCAAGTGCT ACGGCGTGAG CCCCAACCAAG CTGAACGACC TGTGCTTCAC
 · N V Y A D S F V I R G D E V R Q I A P G

1261 CAACGTGTAC GCCGACAGCT TCGTGATCAG AGGCGACGAG GTGAGACAGA TCGCCCCCGG
 · Q T G N I A D Y N Y K L P D D F T G C V
 K417N

1321 CCAGACCGGC AATATCGCCG ACTACAATA CAAGCTGCCC GACGACTTCA CCGGCTGCGT
 · I A W N S N N L D S K V G G N Y N Y L Y

1381 GATCGCGTGG AACAGCAATA ACCTGGACAG CAAGGTGGGC GGCAACTACA ACTACCTCTA
 · R L F R K S N L K P F E R D I S T E I Y

1441 CAGACTGTTC AGAAAGAGCA ACCTGAAGCC CTTGAGAGA GACATCAGCA CCGAGATCTA
 · Q A G S T P C N G V K G F N C Y F P L Q
 E484K

1501 CCAGGCCGGC AGCACCCCTT GCAACGGCGT GAAGGGCTTC AACTGCTACT TCCCCCTCCA
 · S Y G F Q P T Y G V G Y Q P Y R V V V L
 N501Y

1561 GAGCTACGGC TTCCAGCCCA CCTACGGCGT GGGCTACCAG CCCTACAGAG TGGTGGTCTT
 · S F E L L H A P A T V C G P K K S T N L

1621 GAGCTTCGAG CTGCTGCACG CCCCCGCCAC CGTGTGCGGC CCAAGAAGA GCACCAATCT
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Figure 56 continued

· S P A R M A G N G G D A A L A L L L L D

3421 CTCTCCTGCG CGGATGGCTG GTAACGGCGG GGACGCTGCC CTGGCCCTGC TGCTGCTGGA  
· R L N Q L E S X M S G K G Q Q Q Q G Q T

3481 CAGACTGAAC CAGCTGGAGA GCAAGATGAG CGGCAAGGGC CAGCAGCAGC AGGGCCAGAC  
· V T K K S A A E A S K K P R Q K R T A T

3541 TGTGACCAAA AAAAGCGCCG CCGAGGCCAG CAAGAAGCCC AGACAGAAGA GAACCGCCAC  
· X A Y N V T Q A F G R R G P E Q T Q G N

3601 CAAGGCCTAC AACGTGACCC AGGCCTTCGG CAGAAGAGGC CCCGAGCAGA CCCAGGGCAA  
· F G D Q E L I R Q G T D Y K H W P Q I A

3661 CTTGCGCGAC CAGGAGCTGA TCAGACAGGG CACCGACTAC AAGCACTGGC CCCAGATCGC  
· Q F A P S A S A F F G M S R I G M E V T

3721 CCAGTTCGCC CCCAGCGCCA GCGCCTTCTT CCGCATGAGC AGAATCGGCA TGGAGGTGAC  
· P S G T W L T Y T G A I K L D D K D P N

3781 CCCCAGCGGC ACCTGGCTGA CCTACACCGG CGCCATCAAG CTGGACGACA AGGACCCCAA  
· F K D Q V I L L N K H I D A Y K T F P P

3841 CTTCAAGGAT CAGGTGATCC TGCTGAACAA GCACATCGAC GCCTACAAGA CCTTCCCCC  
· T E P K K D K X K K A D E T Q A L P Q R

3901 CACCGAGCCC AAGAAGGACA AGAAGAAGAA GGCCGACGAG ACCCAGGCC TGGCCCGAGAG  
· Q K K Q Q T V T L L P A A D L D D F S K

3961 ACAGAAGAAG CAGCAGACAG TGACATTGCT GCCCGCCGCC GACCTGGACG ACTTCAGCAA  
· Q L Q Q S M S S A D S T Q A E P K S C D

4021 GCAGCTCCAG CAGAGCATGA GCAGCGCCGA CAGCACCCAG GCCGAGCCCA AATCGTGCGA  
· X T H T C P P C P A P E L L G G P S V F

4081 TAAACGCGAT ACGTGCCCCC CCTGTCCAGC CCCAGAGTTG CTGGGTGGAC CGAGCGTGTT  
· L F P P K P K D T L M I S R T P E V T C

4141 CCTGTTCCCC CCCAAGCCCA AGGACACCCT GATGATCAGC AGAACCCCG AGGTGACCTG  
· V V V D V S H E D P E V K F N W Y V D G

4201 CGTGGTGGTG GACGTGAGCC ACGAGGACCC CGAGGTGAAG TTCAACTGCT ACGTGGACGG  
· V E V H T A W T Q P R E E Q Y N S T Y R

4261 CGTGGAGGTG CACACAGCCT GGACCCAGCC CAGAGAGGAG CAGTACAACA GCACCTACAG  
· V V S V L T V L H Q D W L N G K E Y K C

4321 AGTTGTGTCC GTGCTGACCG TGCTGCACCA GGACTGGCTG AACGGCAAGG AGTACAAGTG  
· X V S N K A L P A P I E K T I S K P K G

4381 CAAGGTGAGC AACAAGGCC TGCCCGCCCC CATCGAGAAG ACCATCAGCA AGCCCAAGGG  
· R A Q T P Q V Y T I P P P R E Q M S K K

4441 CAGAGCCCAG ACACCCAGG TGTAACACCA' ACCCCCCCT' AGAGAACAAA 'TG'CCAAGAA  
· K V S L T C L V T N F F S E A I S V E W

4501 GAAGGTGAGC CTGACCTGCC TGGTGACCAA CTCTTCTCT GAAGCCATCA GTGTGGAGTG  
· E S N G Q P E N N Y K T T P P V L D S D

4561 GGAGAGCAAC GGCCAGCCCG AGAACAACTA CAAGACCACC CCCCCGTGC TGGACAGCGA

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Figure 56 continued

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 · G S F F L Y S K L T V D K S R W Q Q G N
4621 CGGCAGCTTC TTCCTCTACA GCAAGCTGAC CGTGGACAAG AGCAGATGGC AGCAGGGCAA
 · V F S C S V M H E A L H N H Y T Q K S L
4681 CGTGTCTCT TGCAGCGTGA TGCACGAGGC CCTGCACAAC CACTACACCC AGAAGAGCCT
 EcoRI
 PstI
 · S L S P G K *
4741 GAGCCTGAGC CCCGGCAAGT' GAT'GAT'C'IAA AGGGCGAA'T' CGCCCT'IAAG GGCT'AA'T'ICT
 PstI
      ~~~~
4801  GCAGATTTCGA GCATGCATAT AGAGGGCCCG TTAAACCCG CTGATCAGCC TCGACTGTGC
4861  CTTCTAGTTG CCAGCCATCT GTTGT'TTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG
4921  GTGCCACTCC CACTGTCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA
4981  GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG
5041  ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGC TTCTACTGGG CGGTTT'TATG
5101  GACAGCAAGC GAACCGGAAT TGCCAGCTGG GCGGCCCTCT GGTAAAGTTG GGAAGCCCTG
5161  CAAAGTAAAC TGGATGGCTT TCTTGCCGCC AAGGATCTGA TGGCGCAGGG GATCAAGCTC
5221  TGATCAAGAG ACAGGATGAG CCGACCC'TTA GACTCTGTAC TCAGTTCTAT AAACGAGCCA
5281  TTGGATACGA GATCCGTAGA TTGATAAGGG ACACGGAATA TCCCCGGACG CAATAGACGG
5341  ACAGCTTGGT ATCCTGAGCA CAGTCGCGCG TCCGAATCTA GCTCTACTTT AGAGGCCCCG
5401  GATTCTGATG GTCGTAGACC GCAGAACCGA TTGGAGGGAT GCTAGCACTA GTGAGGTGAG
5461  ATTGTGTTTC GCATGCC'TCA CAGGCAGATC TATCAGCACA CAATTGCCCA TTATACGC
```

Figure 57

iSCIB1plus whole plasmid vector sequence (SEQ ID NO: 20)

```
1      GCTGCTTCGC  GATGTACGGG  CCAGATATAC  GCGTTGACAT  TGATTATTGA  CTAGTTATTA
61     ATAGTAATCA  ATTACGGGGT  CATTAGTTCA  TAGCCCATAT  ATGGAGTTCC  GCGTTACATA
121    ACTTACGGTA  AATGGCCCCG  CTGGCTGACC  GCGCAACGAC  CCGCGCCCAT  TGACGTCAAT
181    AATGACGTAT  GTTCCCATAG  TAACGCCAAI  AGGGACTTTT  CATTTGACGT  AATGGGTGGA
241    GTATTTACGG  TAAACTGCCC  ACTTGGCAGT  ACATCAAGTG  TATCATATGC  CAAGTACGCC
301    CCTATTGAC  GTCAATGACG  GTAAATGGCC  CGCCTGGCAT  TATGCCCAGT  ACATGACCTT
361    ATGGGACTTT  CCTACTTGGC  AGTACATCTA  CGTATTAGTC  ATCGCTATTA  CCATGGTGAT
421    GCGGTTTTGG  CAGTACATCA  ATGGGCGTGG  ATAGCGGTTT  GACTCACGGG  GATTTCCAAG
481    TCTCCACCCC  ATTGACGTCA  ATGGGAGTTT  GTTTTGGCAC  CAAAATCAAC  GGGACTTTCC
541    AAAATGTCGT  AACAACCTCC  CCCCATTGAC  GCAAAATGGG  GGTAGGCGTG  TACGGTGGGA
601    GGCTATATA  AGCAGAGCTC  TCTGGCTAAC  TAGAGAACCC  ACTGCTTACT  GGCTTATCGA

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661 AATTAATACG ACTCACTATA GGGAGACCCA AGCTAGCTTG GTACCGAGCT CCGATCCACC
 M G W S C I I L F L V A T A T G V H S D
721 ATGGGATGGA GCTGTATCAT CCTTCTCTTG GTAGCAACAG CTACCGGAGT CCACTCCGAT
 V L M T Q S P L S L P V T P G E P A S I
781 GTGTTGATGA CCCAATCTCC ACTCTCCCTG CCTGTCACTC CTGGGGAGCC AGCCTCGATC
 S C W N R Q L Y P E W T E A Q R L D W Y
841 TCTTGCTGGA ACAGGCAGCT GTATCCAGAG TGGACAGAAG CCCAGAGACT TGACTGGTAT
 L Q K P G Q S P Q L L I Y A N C S V Y D
901 CTGCAGAAAC CAGGCCAGTC TCCACAGCTC CTGATCTACG CCAACTGCAG TGTTTATGAT
 F F V W L H Y Y S V R D T L L G P G R P
961 TTTTGTGTGT GGCTCCATTA TTATTTCTGT AGAGATACAT TATTAGGACC AGGACGCCCC
 Y R G V P D R F S G S G S G T D F T L K
1021 TACAGGGGGG TCCCAGACAG ATTCACTGGC AGTGGATCAG GGACAGATTT CACACTCAAG
 I S R V E A E D T G V Y Y C Q C T E V R
1081 ATCAGCAGAG TGGAGGCTGA GGATACCGGA GTGTATTACT GCCAGTGCAC AGAGGTGCGA
 A D T R P W S G P Y I L R N Q D D R E L
1141 GCCGACACAA GGCCTGGAG TGGTCCCTAC ATCCTACGAA ACCAGGATGA CCGTGAGCTG

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                                     ~~~~~~
1201   TGGCCAAGAA  AATTCTTCTT  CGGTGGAGGC  ACCAAGGTGG  AAATCAAGCG  TACGGTAGCG
      A P S V F I F P P S D E Q L K S G T A S
1261   GCCCATCTG  TCTTCACTTT  CCCGCCATCT  GATGAGCAGT  TGAAATCTGG  AACTGCCCTT
      V V C L L N N F Y P R E A K V Q W K V D
1321   GTTGTGTGCC  TGCTGAATAA  CTTCTATCCC  AGAGAGGCCA  AAGTACAGTG  GAAGGTGGAT
      N A L Q S G N S Q E S V T E Q D S K D S
1381   AACGCCCTCC  AATCGGGTAA  CTCCCAGGAG  AGTGTACAG  AGCAGGACAG  CAAGGACAGC
      T Y S L S S T L T L S K A D Y E K H K V
1441   ACCTACAGCC  TCAGCAGCAC  CTTGACGCTG  AGCAAAGCAG  ACTACGAGAA  ACACAAAGTC
      Y A C E V T H Q G L S S P V T K S F N R
1501   TACGCCTGCG  AAGTCACCCA  CCAGGGCCTG  AGCTCGCCCG  TCACAAAGAG  CTTCAACAGG

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                                     ~~~~~~
 G E C *
1561 GGAGAGTGT GACTCGAGCA TGCATCTAGA GGGCCCTATT CTATAGTGTC ACCTAAATGC
1621 TAGAGCTCG TGATCAGCCT CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC
1681 CTCCCCCGT CTTTCTTGA CCTGGAAGG TGCCACTCCC ACTGTCTTTT CCTAATAAAA
1741 TGAGGAAAT GCATCGCAT GTCTGAGTAG GTGTCATTCT ATTCTGGGGG GTGGGGTGGG
1801 GCAGGACAG AAGGGGGAG ATTGGGAAGA CAATAGCAGG CATGCTGGGG ATGCGGTGGG
1861 CTCTATGGCT TCTGAGGCG AAAGAACCAG GCTAGCGTTC GATGTACGGG CCAGATATAC
1921 GCGTTGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA ATTACGGGGT CATTAGTTCA
1981 TAGCCCATAT ATGGAGTTCC GCGTTACATA ACTTACGGTA AATGGCCCCG CTGGCTGACC
2041 GCGCAACGAC CCGCGCCCAT TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT
2101 AGGGACTTTC CATTGACGTC AATGGGTGGA GTATTTACGG TAAACTGCCC ACTTGGCAGT
2161 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG GTAAATGGCC
2221 CGCTGGCAT TATGCCCAGT ACATGACCTT ATGGGACTTT CCTACTTGGC AGTACATCTA
2281 CGTATTAGTC ATCGCTATT CCAATGGTGA GCGGTTTGG CAGTACAICA AATGGGCGTG
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Figure 57 continued

```
2341 ATAGCGGTTT GACTCACGGG GATTTCCAAG TCTCCACCCC ATTGACGTCA ATGGGAGTTT
2401 GTTTTGGCAC CAAAATCAAC GGGACTTTCC AAAATGTCGT AACAACTCCG CCCCATTGAC
2461 GCAAATGGGC GGTAGGCGTG TACGGTGGGA GGTCTATATA AGCAGAGCTC TCTGGCTAAC
2521 TAGAGAACCC ACTGCTTACT GGCTTATCGA AATTAATACG ACTCACTATA GGGAGACCCA
 HindIII
      ~~~~~
      M G W S C I I L F L
2581 AGCTGGCTAG CGTTTAAACT TAAGCTTACC ATGGGATGGA GCTGTATCAT CCTCTTCTTG
      V A T A T G V H S Q V Q L V E T G G G L
2641 GTAGCAACAG CTACCGGAGT CCACTCCCAG GTGCAGCTGG TGGAGACTGG GGGAGGCTTA
      I Q P G G S L R M S C G T G R A M L G T
2701 ATCCAGCCTG GAGGGTCCCT GAGAATGTCC TCGGGACAG GCAGGGCAAT GCTGGGCACA
      H T M E V T V Y H W V R Q A P G K G L E
2761 CACACCATGG AAGTGACTGT CTACCATTTG GTTCGGCAGG CTCCGGGGAA GGGGCTGGAG
      W I A Y I G S G G S V Y D F F V W L R F
2821 TGGATCGCAT ACATTGGTAG TGGTGGTAGT GTTTATGATT TTTTGTGTG GCTCCGATTC
      T I S R D N S K N T L Y L Q L N S L R A
2881 ACCATTTCCA GAGACAATAG CAAGAACACC CTGTATTTCG AATGAACAG TCTGAGGGCT
      E D T A V Y Y C A R V P L D C V L Y R Y
2941 GAGGACACAG CCGTGTATTA CTGTACCCGA GTCCCCCTGG ATTGTGTCTT GTATCGATAT
      G S F S V T L D I V Q G W G Q G T T V T
3001 GGTTCCTTTT CCGTCACCCCT GGACATTGTC CAGGGTTGGG GCCAAGGAAC CACGGTCACC
      AfeI
      ~~~~~
 V S S A S T K G P S V F P L A P S S K S
3061 GTCTCCAGCG CTTCACCAA GGGCCCATCG GTCTTCCCC TGGCACCCTC CTCCAAGAGC
 T S G G T A A L G C L V K D Y F P E P V
3121 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG
 T V S W N S G A L T S G V H T F P A V L
3181 ACGTGTCTGT GGAACCTCAG CGCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCTTA
 Q S S G L Y S L S S V V T V P S S S L G
3241 CAGTCTCTAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
 T Q T Y I C N V N H K P S N T K V D K K
3301 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCACGCA ACACCAAGGT GGACAAGAAA
 V E P K S C D K T H T C P P C P A P E L
3361 GTTGAGCCCA AATCTTGTGA CAAAACCTCAC ACATGCCAC CGTGCCAGC ACCTGAATTC
 L G G P S V F L F P P K P K D T L M I S
3421 CTGGGGGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT CATGATCTCC
 R T P E V T C V V V D V S H E D P E V K
3481 CGGACCCCTG AGGTCAATG CGTGGTGGTG GACGTGAGCC ACGAAGACCC TGAGGTCAGG
 F N W Y V D G V E V H T A W T Q P R E E
3541 TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATACAGCCT GGACACAGCC GCGGGAGGAG
 Q Y N S T Y R V V S V L T V L H Q D W L
3601 CAGTACAACA GCAGTACCG TGTGGTCAGC GTCCTCACCG TCCTGCACCA GGACTGGCTG
 N G K E Y K C K V S N K A L P A P I E K
3661 AATGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGCCC TCCCAGCCCC CATCGAGAAA
 T I S K P K G R A Q T P Q V Y T I P P P
3721 ACCATCTCCA AACCAAAGG GAGAGCCCAG ACACCACAGG TGTACACCAT ACCCCACCT
 R E Q M S K K K V S L T C L V T N F F S
3781 CGGGAACAAA TGTCCAAGAA GAAGGTCAGC CTGACCTGCC TGGTCACCAA CTCTCTCTCT
 E A I S V E W E S N G Q P E N N Y K T T
3841 GAAGCCATCA GTGTGGAGTG GGAGAGCAAT GGGCAGCCGG AGAACAAC TAAGACCACG
 P P V L D S D G S F F L Y S K L T V D K
3901 CCTCCCGTGC TGGACTCCGA CGGCTCCCTT TCTCTCTACA GCAAGCTCAC CGTGGACAAG
 S R W Q Q G N V F S C S V M H E A L H N
3961 AGCAGGTGGC AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC
 EcoRV
      ~~~~~
      H Y T Q K S L S L S P G K *
4021 CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GATCTAAAGG GCGATATCGC
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Figure 57 continued

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|------|-------------|--------------------|------------|------------|-------------|------------|
| 4081 | CCTTAAGGCG | GAATTC TGCA | GATTCGAGCA | TGCATCTAGA | GGGCCCCTTT | AAACCCGCTG |
| 4141 | ATCAGCCTCG | ACTGTGCCCT | CTAGTTGCCA | GCCATCTGTT | GTTTGCCCCCT | CCCCCGTGCC |
| 4201 | TTCCTTGACC | CTGGAAGGTG | CCACTCCCAC | TGTCCTTTCC | TAATAAAATG | AGGAAATFGC |
| 4261 | ATCGCATTGT | CTGAGTAGGT | GTCAATCTAT | TCTGGGGGGT | GGGGTGGGGC | AGGACAGCAA |
| 4321 | GGGGGAGGAT | TGGGAAGACA | ATAGCAGGCA | TGCTGGGGAT | GCGGTGGGCT | CTATGGCTTC |
| 4381 | TACTGGGCGG | TTTATATGGAC | AGCAAGCGAA | CCGGAATTGC | CAGCTGGGGC | GCCCTCTGGT |
| 4441 | AAGGTTGGGA | AGCCCTGCAA | AGTAAACTGG | ATGGCTTTCT | TGCCGCCAAG | GATCTGATGG |
| 4501 | CGCAGGGGAT | CAAGCTCTGA | TCAAGAGACA | GGATGAGGAT | CGTTTCGCAT | GATTGAACAA |
| 4561 | GATGGATTCG | ACGCAGGTTT | TCCGGCCGCT | TGGGTGGAGA | GGCTAATTCGG | CTATGACTGG |
| 4621 | GCACAACAGA | CAATCGGCTG | CTCTGATGCC | GCCGTGTTCC | GGCTGTGAGC | GCAGGGGCGC |
| 4681 | CCGGTTCCTT | TTGTCAAGAC | CGACCTGTCC | GGTGCCCTGA | ATGAAC TGCA | AGACGAGGCA |
| 4741 | GCGCGGCTAT | CGTGGCTGGC | CACGACGGGC | GTTCCCTTGC | CAGCTGTGCT | CGACGTTGTC |
| 4801 | ACTGAAGCGC | GAAGGGACTG | GCTGCTATTG | GGCGAAGTGC | CGGGGCAGGA | TCTCCTGTCA |
| 4861 | TCTCACCTTG | CTCCTGCCGA | GAAAGTATCC | ATCATGGCTG | ATGCAATGCG | GCGGCTGCAT |
| 4921 | ACGCTTGATC | CGGCTACCTG | CCCATTCGAC | CACCAAGCGA | AACATCGCAT | CGAGCGAGCA |
| 4981 | CTTACTCGGA | TGGAAGCCCG | TCTTGTGCGT | CAGGATGATC | TGGACGAAGA | GCATCAGGGG |
| 5041 | CTCGCGCCAG | CCGAAGCTGT | CGCCAGGCTC | AAGGCAGGCA | TGCCCCAGCG | CGAGGATCTC |
| 5101 | GTCGTGACCC | ATGGCGATGC | CTGCTTGCCG | AATATCATGG | TGGAAAATGG | CCGCTTTTCT |
| 5161 | GGATTCATCG | ACTGTGGCCG | GCTGGGTGTG | GCGGACCGCT | ATCAGGACAT | AGCGTTGGCT |
| 5221 | ACCCGTGATA | TTGCTGAAGA | GCTTGGCGGC | GAATGGGCTG | ACCGCTTCCT | CGTGCTTTAC |
| 5281 | GGTATCGCCG | CTCCCGATTC | GCAGCGCATC | GCCTTCTATC | GCCTTCTTGA | CGAGTTCTTC |
| 5341 | TGAATTATTA | ACGCTTACAA | TTTCCTGATG | CGGTATTTTC | TCCTTACGCA | TCTGTGCGGT |
| 5401 | ATTTTCACACC | GCATCAGGTG | GCACCTTTTC | GGGAAATGTG | CGCGGAACCC | CTATTTGTTT |
| 5461 | ATTTTCTCTAA | ATACATTCAA | ATATGTATCC | GCTCATGAGA | CAATAACCCCT | GATAAATGCT |
| 5521 | TCAATAATAG | CACGTGCTAA | AACCTCATT | TTAATTTAAA | AGGATCTAGG | TGAAGATCCT |
| 5581 | TTTTGATAAT | CTCATGACCA | AAATCCCTTA | ACGTGAGTTT | TCGTTCCACT | GAGCGTCAGA |
| 5641 | CCCCGTAGAA | AAGATCAAAG | GATCTTCTTG | AGATCCTTTT | TTTCTGCGCG | TAATCTGCTG |
| 5701 | CTTGCAAAACA | AAAAAACCAC | CGCTACCAGC | GGTGGTTTGT | TTGCCCGGATC | AAGAGCTACC |
| 5761 | AACCTCTTTT | CCGAAGGTAA | CTGGCTTCAG | CAGAGCGCAG | ATACCAAATA | CTGTTCTTCT |
| 5821 | AGTGTAGCCG | TAGTTAGGCC | ACCACTTCAA | GAACCTGTGA | GCACCGCCTA | CATACCTCGC |
| 5881 | TCTGCTAATC | CTGTTACCAG | TGGCTGCTGC | CAGTGGCGAT | AAGTCGTGTC | TTACCGGGTT |
| 5941 | GGACTCAAGA | CGATAGTTAC | CGGATAAGGC | GCAGCGGTTC | GGCTGAACGG | GGGGTTCGTG |
| 6001 | CACACAGCCC | AGCTTGGAGC | GAACGACCTA | CACCGAAGTG | AGATACCTAC | AGCGTGAGCT |
| 6061 | ATGAGAAAAG | GCCACGCTTC | CCGAAGGGAG | AAAGGCGGAC | AGGTATCCGG | TAAGCGGCAG |
| 6121 | GGTCGGAACA | GGAGAGCGCA | CGAGGGAGCT | TCCAGGGGGA | AACGCCTGGT | ATCTTTATAG |
| 6181 | TCCGTGTCGG | TTTCGCCACC | TCTGACTTGA | GCGTCGATTT | TTGTGATGCT | CGTCAGGGGG |
| 6241 | GCGGAGCCTA | TGGAAAAACG | CCAGCAACGC | GGCCTTTTTA | CGGTTCCTGG | CCTTTTGCTG |
| 6301 | GCCTTTGTCT | CACATGTTCT | T | | | |

Figure 58

iSCIB1plus whole doggybone (dbDNA) vector sequence (SEQ ID NO: 21)

```
1   GCGTATAATG GACTATTGTG TGCTGATATG TACACCTGAG GACACAGGTA CAGGACTCAG
61  CTTAAGGCTA CATCTTAGCT TACGTCATA GAGGGTCCAC GTTTAGTTTT TAAGATCCAT
121 TGATCTCCTA AACGCTGCAA GATTCGCAAC CTGGAATACT TAGCGCTAGG TCCTAGTGAA
181 GCGGGACTTT TTTTCTAAAG TCGTTGAGAG GAGGAGTCGT CAGACCAGAT AGCTTTGATG
241 TCCTGATCGG AAGGATCGTT GGCCCCGATG TACGGGCCAG ATATACGCGT TGACATTGAT
301 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC CCATATATGG
361 AGTCCGCGT TACATAACTT ACGGTAAATG GCGCGCTGG CTGACCGCCC AACGACCCCC
421 GCCCATTGAC GTCAATAATG ACGTATGTTT CCATAGTAAC GCCAATAGGG ACTTTCCATT
481 GACGTCAATG GGTGGAGTAT TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC
541 ATATGCCAAG TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCCGC TGGCATTTATG
601 CCCAGTACAT GACCTTATGG GACTTTCCCTA CTTGGCAGTA CATCTACGTA TTAGTCATCG
661 CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG GCGTGGATAG CGGTTTGACT
721 CACGGGGATT TCCAAGTCTC CACCCCATG ACGTCAATGG GAGTTTGTIT TGGCACCAAA
781 ATCAACGGGA CTTTCCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGTA
841 GCGGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCTCTG GCTAAGTAGA GAACCCACTG
901 CTTACTGGCT TATCGAAATT AATACGACTC ACTATAGGGA GACCCAAGCT AGCTTGGTAC

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              M   G   W   S   C   I   I   L   F   L   V   A   T   A   T

.
961  CGAGCTCGGA TCCACCATGG GATGGAGCTG TATCATCCTC TTCTTGGTAG CAACAGCTAC
    . G V H   S D V L   M T Q   S P L   S L P V   T P G
.
1021 CGGAGTCCAC TCCGATGTGT TGATGACCCA ATCTCCACTC TCCCTGCCTG TCACTCCTGG
    . E P A   S I S C   W N R   Q L Y   P E W T   E A Q
.
1081 GGAGCCAGCC TCGATCTCTT GCTGGAACAG GCAGCTGTAT CCAGAGTGGA CAGAAGCCCA
    . R L D   W Y L Q   K P G   Q S P   Q L L I   Y A N
.
1141 GAGACTTGAC TGGTATCTGC AGAAACCAGG CCAGTCTCCA CAGCTCCTGA TCTACGCCAA
    . C S V   Y D F F   V W L   H Y Y   S V R D   T L L
.
1201 CTGCAGTGTT TATGATTTTT TTGTGTGGCT CCATTATTAT TCTGTTAGAG ATACATTATT
    . G P G   R P Y R   G V P   D R F   S G S G   S G T
.
1261 AGGACCAGGA CGCCCCTACA GGGGGGTCCC AGACAGATTC AGTGGCAGTG GATCAGGGAC
    . D F T   L K I S   R V E   A E D   T G V Y   Y C Q
.
1321 AGATTTTACA CTCAAGATCA GCAGAGTGGA GGCTGAGGAT ACCGGAGTGT ATTACTGCCA
    . C T E   V R A D   T R P   W S G   P Y I L   R N Q
.
1381 GTGCACAGAG GTGCGAGCCG ACACAAGGCC CTGGAGTGGT CCTACATCC TACGAAACCA
    . D D R   E L W P   R K F   F F G   G G T K   V E I
.
1441 GGATGACCGT GAGCTGTGGC CAAGAAAATT CTTCTTCGGT GGAGGCACCA AGGTGGAATT
    BsiWI
    ~~~~~~
    . X R T   V A A P   S V F   I F P   P S D E   Q L K
.
1501 CAAGCGTACG GTAGCGGCCC CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA
    . S G T   A S V V   C L L   N N F   Y P R E   A K V
.
1561 ATCTGGAACT GCCTCTGTG TGTGCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
    . Q W K   V D N A   L Q S   G N S   Q E S V   T E Q
.
1621 ACAGTGAAG GTGGATAACG CCTCCAATC GGGTAATCC CAGGAGAGTG TCACAGAGCA
    . D S K   D S T Y   S L S   S T L   T L S K   A D Y
.
1681 GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG ACGCTGAGCA AAGCAGACTA
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Figure 58 continued

· E K H K V Y A C E V T H Q G L S S P V T

1741 CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCACCAG GGCCTGAGCT CGCCCCGCAC

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· K S F N R G E C \*

1801 AAAGAGCTTC AACAGGGGAG AGTGTGACT **CGAGCATGCA** TCAAGAGGGC CCTATTCTAT

1861 AGTGTACCTT AAATGCTAGA GCTCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC

1921 CATCTGTTGT TTGCCCCCTC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCACTG

1981 TCCTTTCCTA ATAAATGAG GAAATTGCAT CGCATTTGCT GAGTAGGTGT CATTCCTATC

2041 TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAA' AGCAGGCATG

2101 CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAAG AACCAGGCTA GCGTTCGATG

2161 TACGGGCCAG ATATACGCGT TGACATTGAT TATTGACTAG TTATTAATAG TAATCAATTA

2221 CGGGGTCATT AGTTCATAGC CCATATATGG AGTTCGCGT TACATAACTT ACGGTAATG

2281 GCCGCGCTGG CTGACCGCCC AACGACCCCG CCCATTGAC GTCAATAATG ACGTATGTTT

2341 CCATAGTAAC GCCAATAGGG ACTTTCATT GACGTCAATG GGTGGAGTAT TTACGGTAAA

2401 CTGCCCCTTT GGCAGTACAT CAAGTGTATC ATATGCCAAG TACGCCCCCT ATTGACGTCA

2461 ATGACGGTAA ATGGCCCCGC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA

2521 CTTGGCAGTA CATCTACGTA TTAGTCAICG CTATTACCAT GGTGATGCGG TTTTGGCAGT

2581 ACATCAATGG GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTT

2641 ACGTCAATGG GAGTTTGTTC TGGCACCAA ATCAACGGGA CTTTCCAAA TGTTCGTAACA

2701 ACTCCGCCCC ATTGACGCAA ATGGGCGGTA GCGGTGTACG GTGGGAGGTC TATATAAGCA

2761 GAGCTCTCTG GCTAACTAGA GAACCCACTG CTTACTGGCT TATCGAAATT AATACGACTC

**HindIII**  
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M G W S C

2821 ACTATAGGGA GACCCAAGCT GGCTAGCGTT TAAACTTAAG **CTTACCATGG** GATGGAGCTG

· I I L F L V A T A T G V H S Q V Q L V E

2881 TATCATCCTC TTCTTGGTAG CAACAGCTAC CGGAGTCCAC TCCCAGGTGC AGCTGGTGGA

· T G G G L I Q P G G S L R M S C G T G R

2941 GACTGGGGGA GGCTTAATCC AGCCTGGAGG GTCCCTGAGA ATGTCTTGCG GGACAGGCAG

· A M L G T H T M E V T V Y H W V R Q A P

3001 GGCAATGCTG GGCACACACA CCATGGAAGT GACTGTCTAC CATTGGGTTT GGCAGGCTCC

· G K G L E W I A Y I G S G G S V Y D F F

3061 GGGGAAGGGG CTGGAGTGGA TCGCATACAT TGGTAGTGGT GGTAGTGTTT ATGATTTTTC

· V W L R F T I S R D N S K N T L Y L Q L

3121 TGTGTGGCTC CGATTACCA TTTCCAGAGA CAATAGCAAG AACACCCTGT ATTTGCAATT

· N S L R A E D T A V Y Y C A R V P L D C

3181 GAACAGTCTG AGGGCTGAGG ACACAGCCGT GTATTACTGT GCCCAGTCC CCCTGGATTG

· V L Y R Y G S F S V T L D I V Q G W G Q

3241 TGTTCGTAT CGATATGGTT CCTTTTCCGT CACCCTGGAC ATTGTCCAGG GTTGGGGCCA

· G T T V T V S S A S T K G P S V F P L A

3301 AGGAACCACG GTCACCGTCT CCAGCGCTTC CACCAAGGGC CCATCGTCTT TCCCCCTGGC

· P S S K S T S G G T A A L G C L V K D Y

3361 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA

· F P E P V T V S W N S G A L T S G V H T

3421 CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC

· F P A V L Q S S G L Y S L S S V V T V P

3481 CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC

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Figure 58 continued

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      · S S S L G T Q T Y I C N V N H K P S N T
3541 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC
      · X V D K K V E P K S C D K T H T C P P C
3601 CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCACC GTG
      · P A P E L L G G P S V F L F P P K P K D
3661 CCCAGCACCT GAACTCCTGG GGGGACCGTC AGTCTTCCTC TTCCCCCAA AACCCAAGGA
      · T L M I S R T P E V T C V V V D V S H E
3721 CACCCTCATG ATCTCCCGGA CCCCTGAGGT CACATGCGTG GTGGTGGACG TGAGCCACGA
      · D P E V K F N W Y V D G V E V H T A W T
3781 AGACCCTGAG GTCAAGTTCA ACTGGTACGT GGACGGCGTG GAGGTGCATA CAGCCTGGAC
      · Q P R E E Q Y N S T Y R V V S V L T V L
3841 ACAGCCGCGG GAGGAGCAGT ACAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCCT
      · H Q D W L N G K E Y K C K V S N K A L P
3901 GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGCCCTCCC
      · A P I E K T I S K P K G R A Q T P Q V Y
3961 AGCCCCCATC GAGAAAACCA TCTCCAAACC CAAAGGGAGA GCCCAGACAC CACAGGTGTA
      · T I P P P R E O M S K K K V S L T C L V
4021 CACCATACCC CCACCTCGGG ACAAATGTC CAAGAAGAAG GTCAGCCTGA CCTGCCTGGT
      · T N F F S E A I S V E W E S N G Q P E N
4081 CACCAACTTC TTCTCTGAAG CCATCAGTGT GGAGTGGGAG AGCAATGGGC AGCCGGAGAA
      · N Y K T T P P V L D S D G S F F L Y S K
4141 CAACTACAAG ACCACGCCTC CCGTGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCAA
      · L T V D K S R W Q Q G N V F S C S V M H
4201 GCTCACCGTG GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA
      · E A L H N H Y T Q K S L S L S P G K *
4261 TGAGGCTCTG CACAACCACT ACACGCAGAA GAGCCTCTCC CTGTCTCCGG GTAAATGATC
      EcoRV EcoRI
      ~~~~~ ~~~~~
4321 TAAAGGGCGA TATCGCCCTT AAGGGCGAAT TCTGCAGATT CGAGCATGCA TATAGAGGGC
4381 CCGTTTAAAC CCGCTGATCA GCCTCGACTG TGCCTTCTAG TTGCCAGCCA TCTGTTGTTT
4441 GCCCCTCCCC CGTGCCTTCC TTGACCCCTGG AAGGTGCCAC TCCCACGTGC CTTTCCTAAT
4501 AAAATGAGGA AATTGCATCG CATGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG
4561 TGGGGCAGGA CAGCAAGGGG GAGGATTGGG AAGACAATAG CAGGCATGCT GGGGATGCGG
4621 TGGGCTCTAT GGCTTCTACT GGGCGGTTT ATGGACAGCA AGCGAACCGG AATTGCCAGC
4681 TGGGGCGCCC TCTGGTAAGG TTGGGAAGCC CTGCAAAGTA AACTGGATGG CTTTCTTGCC
4741 GCCAAGGATC TGATGGCGCA GGGGATCAAG CTCTGATCAA GAGACAGGAT GAGCCGACCC
4801 TTAGACTCTG TACTCAGTTC TATAAACGAG CCATTGGATA CGAGATCCGT AGATTGATAA
4861 GGGACACGGA ATATCCCCGG ACGCAATAGA CGGACAGCTT GGTATCCTGA GCACAGTCGC
4921 GCGTCCGAAT CTAGCTCTAC TTTAGAGGCC CCGGATTCTG ATGGTCGTAG ACCGCAGAAC
4981 CGATTGGAGG GATGCTAGCA CTAGTGAGGT GAGATTGTGT TCGGCATGCC TCACAGGCAG
5041 ATCTATCAGC ACACAATTGC CCATTATACG C
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Figure 59

iSCIB2 whole plasmid vector sequence (SEQ ID NO: 22)

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1      GCTGCTTCGC GATGTACGGG CCAGATATAC GCGTTGACAT TGATTATGA CTAGTTATTA
61     ATAGTAATCA ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
121    ACTTACGGTA AATGGCCCGC CTGGCTGACC GCGCAACGAC CCGCGCCCAT TGACGTCAAT
181    AATGACGTAT' GT'CCCATAG 'AACGCCAA' AGGGACT'IT'C CAT'GACGT'C AAT'GGGTGGA
241    GTATTTACGG TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC
301    CCTATTGAC GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT
361    ATGGGACTTT' CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT
421    GCGGTTTTGG CAGTACATCA ATGGGCGTGG ATAGCGGTTT GACTCACGGG GATTTCCAAG
481    TCTCCACCCC ATTGACGTCA ATGGGAGTTT GTTTTGGCAC CAAAATCAAC GGGACTTTCC
541    AAAATGTCGT AACAACTCCG CCCCATTGAC GCAAAATGGGC GGTAGGCGTG TACGGTGGGA
601    GGCTATATA AGCAGAGCTC TCTGGCTAAC TAGAGAACCC ACTGCTTACT GGCTTATCGA

                                     BamHI
                                     ~~~~~~
661    AATTAATACG ACTCACTATA GGGAGACCCA AGCTAGCTTG GTACCGAGCT CCGATCCACC
      M G W S C I I L F L V A T A T G V H S D
721    ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACCGGAGT CCACTCCGAT
      V L M 'T' Q S P L S L P V 'T' P G E P A S I
781    GTGTTGATGA CCCAATCTCC ACTCTCCCTG CCTGTCACTC CTGGGGAGCC AGCCTCGATC
      S C P G V L L K E F T V S G N I L T I R
841    TCTTGCCCAG GGGTGCTTCT GAAGGAGTTC ACTGTGTCCG GCAACATACT GACTATCCGA
      L T A A D H R W Y L Q K P G Q S P Q L L
901    CTGACTGCTG CAGACCACCG CTGGTATCTG CAGAAACCAG GCCAGTCTCC ACAGCTCCTG
      I Y K V S N R F S G V P D R F S G S G S
961    ATCTACAAAG TTTCCAACCG ATT'TTCTGGG GTCCAGACA GATTCACTGG CACTGGATCA
      G T D F T L K I S R V E A E D T G V Y Y
1021   GGGACAGATT TCACACTCAA GATCAGCAGA GTGGAGGCTG AGGATACCGG AGTGTATTAC
      C F Q G S H V P W T F G G G T K V E I K
1081   TGCTTTCAAG GTTCACATGT TCCGTGGACG TTCGGTGGAG GCACCAAGGT GGAAATCAAG
      BsiWI
      ~~~~~~
      R T V A A P S V F I F P P S D E Q L K S
1141   CGTACGGTAG CGGCCCATC TGTCTTCATC TTCCC GCCAT CTGATGAGCA GTTGAAATCT
      G T A S V V C L L N N F Y P R E A K V Q
1201   GGAAGTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG
      W K V D N A L Q S G N S Q E S V T E Q D
1261   TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC AGAGCAGGAC
      S K D S T Y S L S S T L T L S K A D Y E
1321   AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAGC AGACTACGAG
      K H K V Y A C E V T H Q G L S S P V T K
1381   AAACACAAAG TCTACGCCCTG CGAAGTCACC CACCAGGGCC TGAGCTCGCC CGTCACAAAG

                                     XhoI
                                     ~~~~~~
      S F N R G E C *
1441   AGCTTCAACA GGGGAGAGTG TTGACTCGAG CATGCATCTA GAGGGCCCTA TTCTATAGTG
1501   TCACCTAAAT GCTAGAGCTC GCTGATCAGC CTCGACTGTG CCTTCTAGTT GCCAGCCATC
1561   TGTGTTTTCG CCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT
1621   TTCTTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCAIT' C'ATTC'PGGG
1681   GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA GGCATGCTGG
1741   GGATGCGGTG GGCTCTATGG CTCTGAGGC GGAAGAACC AGGCTAGCGT TCGATGTACG
1801   GGCCAGATAT ACGCGTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG
1861   GTCAATTAGT CATAGCCCAT ATATGGAGT CCGCGTTACA TAACTTACGG TAAATGGCCC
1921   GCTGGCTGA CCGCCCAACG ACCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
1981   AGTAACGCCA ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC
2041   CCACTTGCCA GTACATCAAG TGTATCATAT GCCAAGTACG CCCCTATTG ACGTCAATGA
2101   CGGTAAATGG CCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT TTCTACTTTG
2161   GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT
2221   CAATGGGGCT GGATAGCGGT TTGACTCAGC GGGATTTCCA AGTCTCCACC CCATTGACGT
2281   CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC GTAACAACTC
2341   CGCCCCATTG ACGCAAATGG GCGGTAGCGG TGTACGGTGG GAGGTCTATA TAAGCAGAGC
2401   TCTCTGGCTA ACTAGAGAAC CCACTGCTTA CTGGCTTATC GAAATTAATA CGACTCACIA

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120/121

Figure 59 continued

HindIII
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M G W S C I

2461 TAGGGAGACC CAAGCTGGCT AGCGTTTAAA CTT**AAGCTTA** CCATGGGATG GAGCTGTATC  
I L F L V A T A T G V H S Q V Q L V E T  
2521 ATCCTCTTCT TGGTAGCAAC AGCTACCGGA GTCCACTCCC AGGTGCAGCT GGTGGAGACT  
G G G L I Q P G G S L R M S C L L M W I  
2581 GGGGGAGGCT TAATCCAGCC TGGAGGGTCC CTGAGAATGT CCTGCCTGTT GATGTGGATC  
T Q C F W V R Q A P G K G L E W I A Y I  
2641 ACGCAGTGCT TTTGGGTTTCG GCAGGCTCCG GGAAGGGGC TGGAGTGGAT CGCATACATT  
G S G G S L L M W I T Q C R F T I S R D  
2701 GGTAGTGGTG GTTCCCTGTT GATGTGGATC ACGCAGTGCC GATTCAACAT TTCCAGAGAC  
N S K N T L Y L Q L N S L R A E D T A V  
2761 AATAGCAAGA ACACCCTGTA TTGCAATTG AACAGTCTGA GGGCTGAGGA CACAGCCGTG  
Y Y C A R P E S R L L E F Y L A M P F A  
2821 TATTACTGTG CCCGACCGGA GAGCCGCCTG CTTGAGTTCT ACCTCGCCAT GCCTTTCGCG  
T P M E A E L A R R S L A Q W G Q G T T  
2881 ACACCCATGG AAGCAGAGCT GGCCCGCAG AGCCTGGCCC AGTGGGGCCA AGGAACCACG

**AfeI**  
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2941 V T V S S A S T K G P S V F P L A P S S
GTCACCGTCT CCAGCGCTTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
K S T S G G T A A L G C L V K D Y F P E
3001 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCGGAA
P V T V S W N S G A L T S G V H T F P A
3061 CCGTGACGG TGTCTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
V L Q S S G L Y S L S S V V T V P S S S
3121 GTCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC TCCAGCACC
L G T Q T Y I C N V N H K P S N T K V D
3181 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCAACAAGC CCAGCAACAC CAAGGTGGAC
K K V E P K S C D K T H T C P P C P A P
3241 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCACCCTG CCCAGCACCT
E L L G G P S V F L F P P K P K D T L M
3301 GAACTCCTGG GGGGACCGTC AGTCTTCCTC TTCCCCCAA AACCCAAGGA CACCTCATG
I S R T P E V T C V V V D V S H E D P E
3361 ATCTCCCGGA CCCCTGAGGT CACATGCGTG GTGGTGGACG TGAGCCACGA AGACCTGAG
V K F N W Y V D G V E V H T A W T Q P R
3421 GTCAAGTTCA ACTGGTACGT GGACGGCGTG GAGGTGCATA CAGCCTGGAC ACAGCCCGG
E E Q Y N S T Y R V V S V L T V L H Q D
3481 GAGAGCAGT ACAACAGCAC GTACCGTGTG GTCAGCGTCC TCACCGTCTT CACAGGAC
W L N G K E Y K C K V S N K A L P A P I
3541 TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGCCCTCCC AGCCCCATC
E K T I S K P K G R A Q T P Q V Y T I P
3601 GAGAAAACCA TCTCCAAACC CAAAGGGAGA GCCCAGACAC CACAGGTGTA CACATACCC
P E R E Q M S K K K V S L T C L V T N F
3661 CCACCTCGGG AACAAATGTC CAAGAAGAAG GTCAGCCTGA CCTGCCTGCT CACCAACTTC
F S E A I S V E W E S N G Q P E N N Y K
3721 TTCTCTGAAG CCATCAGTGT GGAGTGGAG AGCAATGGGC AGCCGGAGAA CAACTACAAG
T T P P V L D S D G S F F L Y S K L T V
3781 ACCACGCCTC CCGTGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCAA GCTCACCGTG
D K S R W Q Q G N V F S C S V M H E A L
3841 GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG

EcoRV

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3901 H N H Y T Q K S L S L S P G K \*

CACAACCACT ACACGCAGAA GAGCCTCTCC CTGTCTCCGG GTAAATGATC TAAAGGGCGA

EcoRI

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3961 TATCGCCCTT AAGGGCGAAT TCTGCAGATT CGAGCATGCA TCTAGAGGGC CCGTTTAAAC

4021 CCGTGATCA GCTCGACTG TGCTTCTAG TTGCCAGCA TCTGTTGTTT GCCCTCCCC

SUBSTITUTE SHEET (RULE 26)

Figure 59 continued

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4081   CGTGCCTTCC TTTGACCCTGG AAGGTGCCAC TCCCAC TGTC CTTTCCTAAT AAAATGAGGA
4141   AATTGCATCG CATTTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG TGGGGCAGGA
4201   CAGCAAGGGG GAGGATTGGG AAGACAATAG CAGGCATGCT GGGGATGCGG TGGGCTCTAT
4261   GGCTTCTACT GGGCGGTTTT ATGGACAGCA AGCGAACCGG AATTGCCAGC TGGGGCGCCC
4321   TCTGGTAAGG TTGGGAAGCC CTGCAAAGTA AACTGGATGG CTTTCTTGCC GCCAAGGATC
4381   TGATGGCGCA GGGGATCAAG CTCTGATCAA GAGACAGGAT GAGGATCGTT TCGCATGATT
4441   GAACAAGATG GATTGCACGC AGTTCTCCG GCCGCTTGGG TGGAGAGGCT ATTCTGGCTAT
4501   GACTGGGCAC AACAGACAAT CGGCTGCTCT GATGCCGCGG TGTTCGGCT GTTCAGCGCAG
4561   GGGCGCCCGG TTTCTTTTGT CAAGACCGAC CTGTCCGGTG CCTGAATGA ACTGCAAGAC
4621   GAGGCAGCGC GGTATCGTG GCTGGCCACG ACGGGCGTTC CTTGCGCAGC TGTGCTCGAC
4681   GLTTGTCAC TG AAGCGGGAAG GGACTGGCTG CTTATTGGCG AAGTGCCGGG GCAGGATCTC
4741   CTGTCATCTC ACCTTGCTCC TGCCGAGAAA GTATCCATCA TGGCTGATGC AATGCGCGCG
4801   CTGCATACGC TTGATCCGGC TACCTGCCCA TTCGACCACC AAGCGAAACA TCGCATCGAG
4861   CGAGCACGTA CTCGGATGGA AGCCGGTCTT GTCGATCAGG ATGATCTGGA CGAAGAGCAT
4921   CAGGGGCTCG CGCCAGCCGA ACTGTTCCGC AGGCTCAAGG CGAGCATGCC CGACGGCGAG
4981   GATCTCGTCG TGACCCATGG CGATGCCTGC TTGCCGAATA TCATGGTGGA AAATGGCCGC
5041   TTTTCTGGAT TCATCGACTG TGCCCGGCTG GGTGTGGCGG ACCGCTATCA GGACATAGCG
5101   TTGGCTACCC GTGATATTGC TGAAGAGCTT GCGGCGGAAT GGGCTGACCG CTTCTCTCGT
5161   CTTTACGGTA TCGCCGCTCC CGATTGCGAG CGCATCGCT TCTATCGCT TCTTGACGAG
5221   TTCTTCTGAA TTATTAACGC TTACAATTTC CTGATGCGGT ATTTTCTCCT TACGCATCTG
5281   TGCGGTATTT CACACCGCAT CAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT
5341   TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCCTGATA
5401   AATGCTTCAA TAATAGCAG TGCTAAAAC TCAATTTTAA TTTAAAAGGA TCTAGGTGAA
5461   GATCCTTTTT GATAATCTCA TGACCAAAAT CCTTAACGT GAGTTTTCTG TCCACTGAGC
5521   GTCAGACCCC GTAGAAAAGA TCAAAGGATC TTCTTGAGAT CTTTTTTTTT TGC GCGTAAT
5581   CTGCTGCTTG CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA
5641   GCTACCAACT CTTTTTCCGA AGGTAAC TGG CTTGAGCAGA GCGCAGATAC CAAATACTGT
5701   TCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC TCTGTAGCAC CGCTACATA
5761   CCTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GCGGATAAGT CGTGTCTTAC
5821   CGGGTTGGAC TCAAGACGAT AGTTACCGGA TAAGGCGCAG CGGTGCGGCT GAACGGGGGG
5881   TTCTGTCACA CAGCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG
5941   TGAGCTATGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT ATCCGGTAAG
6001   CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA GGGGAAACG CCTGGTATCT
6061   TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTGT GATGCTCGTC
6121   AGGGGGGCGG AGCCTATGGA AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT
6181   TTGCTGGCT TTTGCTCACA TGTCTT
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